

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:13:22 ; Search time 94.2857 Seconds
(without alignments)

87.287 Million cell updates/sec

Title: US-10-712-447-2

Perfect score: 98

Sequence: 1 GIRRFLGSIWRIFAFVG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_8:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

9: Geneseqp2005s:*

10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	18	ADO34231	Synthetic
2	98	100.0	18	ADO34225	Synthetic
3	98	100.0	18	ADO34228	Synthetic
4	98	100.0	18	ADO34236	Synthetic
5	98	100.0	18	ADO34233	Synthetic
6	95	96.9	18	ADO34314	Synthetic
7	94	95.9	18	ADO34354	Synthetic
8	94	95.9	18	ADO34338	Synthetic
9	94	95.9	18	ADO34352	Synthetic
10	94	95.9	18	ADO34340	Synthetic
11	94	95.9	18	ADO34339	Synthetic
12	92	93.9	18	ADO34297	Synthetic
13	92	93.9	18	ADO34244	Synthetic
14	92	93.9	18	ADO34276	Synthetic
15	90	91.8	18	ADO34227	Synthetic
16	90	91.8	18	ADO34350	Synthetic
17	89	90.8	18	ADO34322	Synthetic
18	88	89.8	18	ADO34336	Synthetic
19	88	89.8	18	ADO34335	Synthetic
20	88	89.8	18	ADO34337	Synthetic
21	88	89.8	18	ADO34241	Synthetic
22	87	88.8	18	ADO34240	Synthetic
23	86	87.8	18	ADO34284	Synthetic

24	86	87.8	18	8	ADO34305	Synthetic
25	85	86.7	18	8	ADO34239	Synthetic
26	85	86.7	18	8	ADO34344	Synthetic
27	85	86.7	18	8	ADO34319	Synthetic
28	84	85.7	18	8	ADO34245	Synthetic
29	84	85.7	18	8	ADO34301	Synthetic
30	84	85.7	18	8	ADO34343	Synthetic
31	84	85.7	18	8	ADO34318	Synthetic
32	82	83.7	18	8	ADO34302	Synthetic
33	82	83.7	18	8	ADO34279	Synthetic
34	82	83.7	18	8	ADO34303	Synthetic
35	82	83.7	18	8	ADO34242	Synthetic
36	82	83.7	18	8	ADO34300	Synthetic
37	82	83.7	18	8	ADO34281	Synthetic
38	82	83.7	18	8	ADO34317	Synthetic
39	81	82.7	18	8	ADO34323	Synthetic
40	81	82.7	18	8	ADO34280	Synthetic
41	80	81.6	18	8	ADO34264	Synthetic
42	79	80.6	18	8	ADO34320	Synthetic
43	78	79.6	18	2	AAI18917	Lecithin:
44	78	79.6	18	2	AAI19171	Lecithin:
45	78	79.6	18	2	AAI19425	Lecithin:

ALIGNMENTS

RESULT 1

ID ADO34231 standard; peptide; 18 AA.

XX ADO34231;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 8.

apolipoprotein-E mimicking polypeptide; antilipemic; cardiac;
vasotropic; antiarteriosclerotic; cerebroprotective; antidiabetic;
serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
atherosclerosis; myocardial infarction; stroke; embolus; angina;
low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

PN WO2004043403-A2.

XX 27-MAY-2004.

PF 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

FA (UABR-) UAB RES FOUND.

PI Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
coronary artery disease, dysbetalipoproteinemia or atherosclerosis
comprises an amino acid sequence.

PS Claim 4; SEQ ID NO 8; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
polypeptide. The invention further comprises an isolated nucleic acid
encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
a host cell, a recombinant cell or a transgenic, non-human subject
(including animal or plant) comprising the synthetic apolipoprotein-E
mimicking polypeptide encoding polynucleotide; a composition comprising
the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18
 |||||
 Db 1 GIRRFLGSIWRFIRAFYG 18
 |||||

RESULT 2
 ADO34225
 ID ADO34225 standard; peptide; 18 AA.
 XX
 AC ADO34225;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Synthetic apolipoprotein-E mimicking polypeptide related R18L peptide.
 XX
 KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 18 /note= "C-terminal amide"
 FT
 XX WO2004043403-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 13-NOV-2003; 2003WO-US036268.
 XX
 PR 13-NOV-2002; 2002US-0425821P.
 XX
 PA (UABR-) UAB RES FOUND.
 XX
 PI Anantharamiah GM, Garber DW, Datta G;
 XX
 DR WPI; 2004-411629/38.
 XX
 XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.
 XX
 PS Claim 4; SEQ ID NO 2; 79pp; English.
 XX
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 .CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,

CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18
 |||||
 Db 1 GIRRFLGSIWRFIRAFYG 18
 |||||

RESULT 3
 ADO34228
 ID ADO34228 standard; peptide; 18 AA.
 XX
 AC ADO34228;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 5.
 XX
 KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
 XX
 OS Synthetic.
 XX
 PN WO2004043403-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 13-NOV-2003; 2003WO-US036268.
 XX
 PR 13-NOV-2002; 2002US-0425821P.
 XX
 PA (UABR-) UAB RES FOUND.
 XX
 PI Anantharamiah GM, Garber DW, Datta G;
 XX
 DR WPI; 2004-411629/38.
 XX
 XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.
 XX
 PS Claim 4; SEQ ID NO 5; 79pp; English.
 XX
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 .CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,

CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipemic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
 |||||
 Db 1 GRRFLGSIWRFIRAFYG 18

RESULT 4
 ADO34236
 ID ADO34236 standard; peptide; 18 AA.
 XX
 AC ADO34236;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 13.
 XX
 KW apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.
 XX
 XX WO2004043403-A2.
 XX
 XX 27-MAY-2004.
 XX
 XX 13-NOV-2003; 2003WO-US036268.
 XX
 XX 13-NOV-2002; 2002US-0425821P.
 XX
 XX (UABR-) UAB RES FOUND.
 XX
 XX Anantharamiah GM, Garber DW, Datta G;
 XX
 XX WPI; 2004-411629/38.

XX
 XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX
 XX Claim 4; SEQ ID NO 13; 79pp; English.
 XX
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E

CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipemic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
 |||||
 Db 1 GRRFLGSIWRFIRAFYG 18

RESULT 5
 ADO34233
 ID ADO34233 standard; peptide; 18 AA.
 XX
 AC ADO34233;
 XX

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 10.

XX
 KW apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX
 XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX
 XX Claim 4; SEQ ID NO 10; 79pp; English.

XX
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising

CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFIRAFYIG 18
 |||||
 Db 1 GIRRFGLSIWRFIRAFYIG 18

RESULT 6
 ADO34314
 ID ADO34314 standard; peptide; 18 AA.

XX
 AC ADO34314;

XX
 DT 12-AUG-2004 (first entry)

XX
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 91.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX
 OS Synthetic.

XX
 PN WO2004043403-A2.

XX
 PD 27-MAY-2004.

XX
 PF 13-NOV-2003; 2003WO-US036268.

XX
 PR 13-NOV-2002; 2002US-0425821P.

XX
 PA (UABR-) UAB RES FOUND.

XX
 PI Anantharamiah GM, Garber DW, Datta G;

XX
 DR WPI; 2004-411629/38.

XX
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX
 PS Claim 4; SEQ ID NO 91; 79pp; English.

XX
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 SQ Sequence 18 AA;

Query Match 96.9%; Score 95; DB 8; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.8e-07;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFIRAFYIG 18
 |||||
 Db 1 GIRRFGLSIWRFIRAFYIG 18

RESULT 7
 ADO34354
 ID ADO34354 standard; peptide; 18 AA.

XX
 AC ADO34354;

XX
 DT 12-AUG-2004 (first entry)

XX
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 131.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX
 OS Synthetic.

XX
 PN WO2004043403-A2.

XX
 PD 27-MAY-2004.

XX
 PF 13-NOV-2003; 2003WO-US036268.

XX
 PR 13-NOV-2002; 2002US-0425821P.

XX
 PA (UABR-) UAB RES FOUND.

XX
 PI Anantharamiah GM, Garber DW, Datta G;

XX
 DR WPI; 2004-411629/38.

XX
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX
 PS Claim 4; SEQ ID NO 131; 79pp; English.

XX
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 XX
 SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRFLGSIWRPFIRAFYG 18
 |:|||||:|||||
 Db 1 GLRRFLGSIWRFLRAFG 18

RESULT 8
 ADO34338
 ID ADO34338 standard; peptide; 18 AA.

XX
 AC ADO34338;

XX
 DT 12-AUG-2004 (first entry)

XX
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 115.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX
 OS Synthetic.

XX
 PN WO2004043403-A2.

XX
 PD 27-MAY-2004.

XX
 PF 13-NOV-2003; 2003WO-US036268.

XX
 PR 13-NOV-2002; 2002US-0425821P.

XX
 PA (UABR-) UAB RES FOUND.

XX
 PI Anantharamiah GM, Garber DW, Datta G;

XX
 DR WPI; 2004-411629/38.

XX
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX
 PS Claim 4; SEQ ID NO 115; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRFLGSIWRPFIRAFYG 18
 |:|||||:|||||
 Db 1 GLRRFLGSIWRFLRAFG 18

RESULT 9
 ADO34352
 ID ADO34352 standard; peptide; 18 AA.

XX
 AC ADO34352;

XX
 DT 12-AUG-2004 (first entry)

XX
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 129.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX
 OS Synthetic.

XX
 PN WO2004043403-A2.

XX
 PD 27-MAY-2004.

XX
 PF 13-NOV-2003; 2003WO-US036268.

XX
 PR 13-NOV-2002; 2002US-0425821P.

XX
 PA (UABR-) UAB RES FOUND.

XX
 PI Anantharamiah GM, Garber DW, Datta G;

XX
 DR WPI; 2004-411629/38.

XX
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX
 PS Claim 4; SEQ ID NO 129; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,

CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antiangular. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFTRAFYG 18
 |||||:||||:||||
 Db 1 GIRRFGLSIWRFTRAFYG 18

RESULT 10
 ADO34340
 ID ADO34340 standard; peptide; 18 AA.

XX ADO34340;

DT 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 117.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antiangular;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

PN 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

DR WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 117; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

CC antiangular. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFTRAFYG 18
 |||||:||||:||||
 Db 1 GIRRFGLSIWRFTRAFYG 18

RESULT 11
 ADO34339
 ID ADO34339 standard; peptide; 18 AA.

XX ADO34339;

XX 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 116.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antiangular;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

PN 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

DR WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 116; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antiangular. The synthetic apolipoprotein-E mimicking polypeptide is

polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and a monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipemic, cardiant, vasotropic, antiatherosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,

CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 93.9%; Score 92; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 5.3e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYV 18
 ||:|||||:|||||:|||||
 Db 1 GIRRFLGAIWRFIRSFYV 18

RESULT 14

ADO34276 ID ADO34276 standard; peptide; 18 AA.

XX ADO34276;

DT 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 53.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
 XX Synthetic.

OS Key Location/Qualifiers

FN Modified-site 1.18 /note= "All Lys residues are DiMethyl-Lysine"

PN WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

DR WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

PS Claim 4; SEQ ID NO 53; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 93.9%; Score 92; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 5.3e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYV 18
 ||:|||||:|||||:|||||
 Db 1 GIRRFLGSIWRFIRAFYV 18

RESULT 15

ADO34227 ID ADO34227 standard; peptide; 18 AA.

XX ADO34227;

XX 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking related R18L linear peptide.
 DE apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

PS Claim 4; SEQ ID NO 4; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

xx

SQ Sequence 18 AA;

Query Match 91.8%; Score 90; DB 8; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.1e-06;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GRRFLGSIWRFIRAFVG 18

Db 1 GRRFLGSIWRFIRAFVG 18

Search completed: May 19, 2006, 14:24:30
 Job time : 94.2857 secs

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:24:57 ; Search time 14.2857 Seconds
(without alignments)
121.233 Million cell updates/sec

Title: US-10-712-447-2

Perfect score: 98

Sequence: 1 GIRRFLGSIWRFTRAFVG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	49.0	627	2	S76462
2	45	45.9	178	2	A75578
3	44	44.9	461	1	G64537
4	44	44.9	589	2	A34341
5	44	44.9	806	2	A84060
6	44	44.9	861	2	H64102
7	43.5	44.4	1025	2	A83568
8	43	43.9	265	2	T32316
9	43	43.9	489	2	B84733
10	43	43.9	516	2	T33269
11	43	43.9	812	2	A46417
12	43	43.9	1607	2	T04583
13	42.5	43.4	407	2	T12085
14	42.5	43.4	760	2	E84953
15	42	42.9	107	2	T52113
16	42	42.9	214	2	D72540
17	42	42.9	228	2	T15530
18	42	42.9	237	2	B72692
19	42	42.9	246	2	I54412
20	42	42.9	258	2	F71707
21	42	42.9	273	1	HLHU69
22	42	42.9	365	1	HLHUA2
23	42	42.9	365	2	I38443
24	42	42.9	365	2	I61902
25	42	42.9	365	2	I37542
26	42	42.9	365	2	I84448
27	42	42.9	365	2	I61857
28	42	42.9	365	2	I38442
29	42	42.9	365	2	I38442

30	42	42.9	537	2	T04745
31	42	42.9	803	2	AD1282
32	42	42.9	803	2	AH1653
33	42	42.9	804	2	B89961
34	42	42.9	804	2	D69650
35	41.5	42.3	790	2	T50337
36	41	41.8	131	2	AG2115
37	41	41.8	265	2	C42595
38	41	41.8	279	2	E64109
39	41	41.8	359	2	T20575
40	41	41.8	364	2	AF2599
41	41	41.8	364	2	G97381
42	41	41.8	384	2	T08940
43	41	41.8	406	2	F96571
44	41	41.8	503	2	D96776
45	41	41.8	519	1	T02263

ALIGNMENTS

RESULT 1

S76462 hypothetical protein - Synchocystis sp. (strain PCC 6803)

C;Species: Synchocystis sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C;Accession: S76462

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,

DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis

s.

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S76462

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-627 <KAN>

A;Cross-references: UNIPROT:P74489; UNIPARC:UPI00000C103F; EMBL:D90915; GB:AB001339; NID:

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 49.0%; Score 48; DB 2; Length 627;

Best Local Similarity 38.9%; Pred. No. 8.1;

Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFTRAFVG 18

Db 597 GLEQLLQKIQWLQKFG 614

RESULT 2

A75578

transcription regulator, MarR family - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: A75578

R;White, O.; Bisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma,

Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A;Reference number: A75250; MUID:20036896; PMID:10567266

A;Accession: A75578

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-178 <WHI>

A;Cross-references: UNIPROT:Q9YR0; UNIPARC:UPI00000D3BE4; GB:AE001863; NID:

A;Experimental source: strain R1

C;Genetics:

A;Gene: DRA0248

A;Map position: 2

Query Match 45.9%; Score 45; DB 2; Length 178;

Best Local Similarity 69.2%; Pred. No. 7.2; Mismatches 0; Indels 4; Gaps 0;
Matches 9; Conservative 0

QY 2 IRFLGSIWRFIR 14
| | | | |
Db 23 ILRFLGGIWRNLR 35

RESULT 3
G64537
2-oxoglutarate/malate translocator - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: G64537
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:9739467; PMID:9252185
A;Accession: G64537
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-461 <TOM>
A;Cross-references: UNIPARC:UPI0000174217; GB:AE000511; TIGR:HP0143
C;Superfamily: 2-oxoglutarate/malate translocator

Query Match 44.9%; Score 44; DB 1; Length 461;
Best Local Similarity 53.8%; Pred. No. 26; Mismatches 2; Indels 4; Gaps 0;
Matches 7; Conservative 0

QY 2 IRFLGSIWRFIR 14
: | | | | |
Db 297 VRLLSFWRFVR 309

RESULT 4
A34341
poly(3-hydroxybutyrate) synthase (EC 2.3.1.-) - Alcaligenes eutrophus
C;Species: Alcaligenes eutrophus
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C;Accession: A34341; A39190
R;Peoples, O.P.; Sinskey, A.J. J. Biol. Chem. 264, 15298-15303, 1989
A;Title: Poly-beta-hydroxybutyrate (PHB) biosynthesis in Alcaligenes eutrophus H16. Ident
A;Reference number: A34341; MUID:89359357; PMID:2670936
A;Accession: A34341
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-589 <PEO>
A;Cross-references: UNIPROT:P23608; UNIPARC:UPI0000044953; GB:J05003; NID:g141958; PIDN:R;Schubert, P.; Krueger, N.; Steinbuechel, A. J. Bacteriol. 173, 168-175, 1991
A;Title: Molecular analysis of the Alcaligenes eutrophus poly(3-hydroxybutyrate) biosynt
omoter.
A;Reference number: A39190; MUID:91100279; PMID:1987116
A;Accession: A39190
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-219 <SCH>
A;Cross-references: UNIPARC:UPI000016E162; GB:M64341; NID:g141964; PIDN:AAA21979.1; PID: A;Note: the authors translated the codon TAC for residue 120 as Thr
C;Superfamily: poly(3-hydroxyalkanoic acid) synthase phbC
C;Keywords: acyltransferase

Query Match 44.9%; Score 44; DB 2; Length 589;
Best Local Similarity 47.6%; Pred. No. 33; Mismatches 5; Indels 6; Gaps 1;
Matches 10; Conservative 0

QY 3 RRFGLSIW-----RIFRIFY 17
| | | | |

Db 100 RRFAGDAWETNLPYRFAAAFY 120

RESULT 5
A84060
leucyl-tRNA synthetase leus [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: A84060
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A84060
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-806 <STO>
A;Cross-references: UNIPROT:Q9K788; UNIPARC:UPI0000136555; GB:AP001518; GB:BA000004; NID: A;Experimental source: strain C-125
C;Genetics:
A;Gene: leus
C;Superfamily: leucine-tRNA ligase

Query Match 44.9%; Score 44; DB 2; Length 806;
Best Local Similarity 53.8%; Pred. No. 45; Mismatches 2; Indels 4; Gaps 0;
Matches 7; Conservative 0

QY 1 GRRFLGSIWRFI 13
| | | | |
Db 622 GARRFLDRVWRL 634

RESULT 6
H64102
leucine-tRNA ligase (EC 6.1.1.4) - Haemophilus influenzae (strain Rd KW20)
N;Alternate names: leucyl-tRNA synthetase
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: H64102
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C.
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: H64102
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-861 <TIGR>
A;Cross-references: UNIPROT:P43827; UNIPARC:UPI000013655F; GB:U32774; GB:U42023; NID:g15: C;Genetics:
A;Gene: leus
C;Superfamily: leucine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 44.9%; Score 44; DB 2; Length 861;
Best Local Similarity 46.2%; Pred. No. 48; Mismatches 3; Indels 4; Gaps 0;
Matches 6; Conservative 0

QY 1 GRRFLGSIWRFI 13
| | | | |
Db 665 GAKRFLGRVWNLV 677

RESULT 7
AH3568
acriflavin resistance protein F [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AH3568
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, I.
; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letescac

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
A;Reference number: AD3252; PMID:11756688
A;Accession: AH3568
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1025 <KUR>
A;Cross-references: UNIPROT:Q8YCO5; UNIPARC:UPI00000584C8; GB:AE008918; PIDN:AAL53715.1
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI10473
A;Map position: II
C;Superfamily: hypothetical protein b2075

Query Match 44.4%; Score 43.5; DB 2; Length 1025;
Best Local Similarity 50.0%; Pred. No. 69;
Matches 8; Conservative 4; Mismatches 1; Indels 3; Gaps 1;

QY 5 FLGSIMRFI---RAFY 17
||||| | | | |
Db 531 FLGSVWSFMTLPRSF 546

RESULT 8
T32316
hypothetical protein F31F4.4 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Dec-2004
C;Accession: T32316
R;Blanchard, M.; Kramer, J.; Elliott, G.; Twyman, B.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of *C. elegans* cosmid F31F4.
A;Reference number: Z21149
A;Accession: T32316
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-265 <BLA>
A;Cross-references: UNIPROT:O17136; UNIPARC:UPI000007D19A; EMBL:AF024503; PIDN:AAB70384.
A;Experimental source: strain Bristol N2; clone F31F4
C;Genetics:
A;Gene: CESP:F31F4.4
A;Map position: 5
A;Introns: 13/3; 67/2
C;Superfamily: *Caenorhabditis elegans* hypothetical protein T09F5.1

Query Match 43.9%; Score 43; DB 2; Length 265;
Best Local Similarity 53.8%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 LGSIMRFIRAFYG 18
||| | | | |
Db 253 LASLWAFVHAPEG 265

RESULT 9
B84733
Probable cytochrome P450 [imported] - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B84733
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
Euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A;Reference number: B84420; MUID:20083487; PMID:10617197
A;Accession: B84733
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-489 <STO>
A;Cross-references: UNIPROT:Q9ZV72; UNIPARC:UPI000009D8ED; GB:AE002093; NID:G3831452; PI
C;Genetics:
A;Gene: At2g32440

A;Map position: 2
C;Superfamily: *Synechocystis* cytochrome P450 slr0574; cytochrome P450 homology

Query Match 43.9%; Score 43; DB 2; Length 489;
Best Local Similarity 54.5%; Pred. No. 40;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 LGSIMRFIRAF 16
||| | | | |
Db 54 IGNMWSFLRAF 64

RESULT 10
T33269
hypothetical protein C24B9.13 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33269
R;Murray, J.; Wohldmann, P.; Langston, Y.; O'Neal, D.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of *C. elegans* cosmid C24B9.
A;Reference number: Z21310
A;Accession: T33269
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-516 <MUR>
A;Cross-references: UNIPROT:O76442; UNIPARC:UPI000007D477; EMBL:AF068709; PIDN:AAC19257.1
A;Experimental source: strain Bristol N2; clone C24B9
C;Genetics:
A;Gene: CESP:C24B9.13
A;Map position: 5
A;Introns: 13/3; 67/2; 116/2; 268/2; 315/2; 364/2.

Query Match 43.9%; Score 43; DB 2; Length 516;
Best Local Similarity 41.2%; Pred. No. 42;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 IRRFLGSIMRFIRAFYG 18
||| | | | |
Db 252 LKFFITSLNMFMHAFDG 268

RESULT 11
A46417
NIP1 protein - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: nuclear import protein; protein YM9924.01c; protein YM9952.11c; protei
C;Species: *Saccharomyces cerevisiae*
C;Date: 21-Sep-1993 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A46417; S53979; S59302
R;Gu, Z.; Moersschell, R.P.; Sherman, F.; Goldfarb, D.S.
Proc. Natl. Acad. Sci. U.S.A. 89, 10355-10359, 1992
A;Title: NIP1, a gene required for nuclear transport in yeast.
A;Reference number: A46417; MUID:93066237; PMID:1332047
A;Accession: A46417
A;Molecule type: DNA
A;Residues: 1-812 <GUL>
A;Cross-references: UNIPROT:P32497; UNIPARC:UPI000017B2E1; EMBL:I02899
A;Note: sequence extracted from NCBI backbone (NCBIN:117849, NCBI:P:117850)
R;Connor, R.; Churcher, C.M.
submitted to the EMBL Data Library, April 1995
A;Reference number: S53969
A;Accession: S53979
A;Molecule type: DNA
A;Residues: 571-582, 'Q', 584-640, 'K', 642, 'K', 644-812 <CON>
A;Cross-references: UNIPARC:UPI0000168ACD; EMBL:Z49212; NID:G798940; PID:G798951; MIPS:Y
R;Churcher, C.M.
submitted to the EMBL Data Library, September 1995
A;Reference number: S59302
A;Accession: S59302
A;Molecule type: DNA
A;Residues: 1-110, 'V', 112-582, 'Q', 584-602 <CHU>
A;Cross-references: UNIPARC:UPI0000168ACA; EMBL:Z54141; NID:G1072408; PID:G984682; MIPS:Y
A;Experimental source: strain AB972

C;Genetics:

A;Gene: SGD:NIP1

A;Cross-references: SGD:S0004926; MIPS:YMR309C

A;Map position: 13R

Query Match

Best Local Similarity 43.9%; Score 43; DB 2; Length 812;

Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 GIRFLGSIRRFI 13

: : | | | | | : :

361 GVXRLGSIFSIV 373

RESULT 12

T04583

TMV resistance protein N homolog F23E13.30 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: T04583; T05507

R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Dueterhoeft, A.; Jesse, T.

submitted to the Protein Sequence Database, March 1998

A;Reference number: Z15378

A;Accession: T04583

A;Molecule type: DNA

A;Residues: 1-1607 <BEV>

A;Cross-references: UNIPROT:O65506; UNIPARC:UPI00000AA45C; EMBL:AL022141

A;Experimental source: cultivar Columbia; BAC clone F23E13

R;Bevan, M.; Wedler, H.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schueller

submitted to the Protein Sequence Database, April 1998

A;Reference number: Z15418

A;Accession: T05507

A;Molecule type: DNA

A;Residues: 1448-1607 <BE2>

A;Cross-references: UNIPARC:UPI000016DBPD; EMBL:AL022373

A;Experimental source: cultivar Columbia; BAC clone T19K4

C;Genetics:

A;Map position: 4

A;Introns: 193/2; 238/2; 556/2; 930/3; 1029/3; 1287/3

A;Note: F23E13.30; T19K4.270

Query Match

Best Local Similarity 43.9%; Score 43; DB 2; Length 1607;

Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 LGSIWRFIRAF 16

: : | | | | | : :

Db 1321 LGSSWRLIRGF 1331

RESULT 13

T12085

reverse transcriptase homolog - fava bean (fragment)

C;Species: Vicia faba (fava bean)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C;Accession: T12085

R;Kinoshita, T.; Wada, H.; Masaaki, I.; Shimazaki, K.

submitted to the EMBL Data Library, September 1997

A;Description: Retrotransposon-like cDNAs from guard cell protoplasts in Vicia faba.

A;Reference number: Z17406

A;Accession: T12085

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-407 <KIN>

A;Cross-references: UNIPROT:O22103; UNIPARC:UPI00000AAD3D; EMBL:AB007466; NID:d1170509;

A;Experimental source: guard cell protoplasts

C;Superfamily: pol polyprotein

Query Match

Best Local Similarity 43.4%; Score 42.5; DB 2; Length 407;

Matches 11; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

QY 1 GIRFLGSIN---RFIRAF 16

: : | | | | | : :

Db 178 GIRSFLGHVGYRRFIRDF 196

RESULT 14

E84953

penicillin-binding protein 1b [imported] - Buchnera sp. (strain APS)

C;Species: Buchnera sp.

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002

C;Accession: E84953

R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.

Nature 407, 81-86, 2000

A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. AI

A;Reference number: A84930; MUID:20445173; PMID:10993077

A;Accession: E84953

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-760 <STO>

A;Cross-references: UNIPARC:UPI000005E4C8; GB:AP000398; GSPDB:GN00144

A;Experimental source: strain APS

C;Genetics:

A;Gene: mrcB; BU200

C;Superfamily: penicillin-binding protein 1B

Query Match

Best Local Similarity 43.4%; Score 42.5; DB 2; Length 760;

Matches 8; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 2 IRRFL-GSIWRFIRAFY 18

: : | | | | | : :

Db 32 INRFINGKVNFPPTSIYG 49

RESULT 15

T52113

probable transcription co-activator KIWI [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004

C;Accession: T52113

R;Cornack, R.S.; Hahlbrock, K.; Somssich, I.E.

Plant J. 14, 685-92, 1998

A;Title: Isolation of putative plant transcriptional coactivators using a modified two-h

A;Reference number: Z25848; MUID:98346011; PMID:9681033

A;Accession: T52113

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-107 <COR>

A;Cross-references: UNIPROT:O65154; UNIPARC:UPI000000C45F; EMBL:AF053302; PIDN:AAC08574.J

A;Experimental source: cultivar Columbia

C;Genetics:

A;Gene: KIWI

A;Map position: V

C;Function:

A;Description: probably plays a role in gene activation during pathogen defence and plant

C;Superfamily: Caenorhabditis elegans hypothetical protein T13F2.2

Query Match

Best Local Similarity 42.9%; Score 42; DB 2; Length 107;

Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 IRRFLGSIWRFIRAFY 17

: : | | | | | : :

Db 54 VRNNGKIWIIDREFY 69

Search completed: May 19, 2006, 14:39:56

Job time : 14.2857 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:13:32 ; Search time 115.429 Seconds
(without alignments)
144.247 Million cell updates/sec

Title: US-10-712-447-2

Perfect score: 98

Sequence: 1 GIRRFLGSIWRIFAFVG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	59.2	805	Q3APY5_CHLCH	Q3apY5 chlorobium
2	54	55.1	670	Q25271_LEPDE	Q25271 leptinotars
3	52	53.1	735	Q9F7V7_RHILV	Q9f7v7 rhizobium 1
4	52	53.1	805	Q44QD1_CHLLB	Q44qdl chlorobium
5	52	53.1	816	Q43K01_9CHLB	Q43k01 chlorobium
6	51	52.0	407	Q39L57_BURS3	Q39l57 burkholderi
7	51	52.0	408	Q456F4_9BURK	Q456f4 burkholderi
8	51	52.0	408	Q4LK44_9BURK	Q4lk44 burkholderi
9	50	51.0	579	1_XKR7_HUMAN	Q5gh72 homo sapien
10	50	51.0	579	1_XKR7_PANTR	Q49lsl pan troglod
11	50	51.0	580	1_XKR7_MOUSE	Q5gh64 mus musculu
12	50	51.0	580	1_XKR7_RAT	Q5gh56 rattus norv
13	49	50.0	409	Q48FM2_BURVI	Q4bfm2 burkholderi
14	49	50.0	449	Q3PK79_PARDE	Q3pk79 paracoccus
15	49	50.0	488	Q84ZWI_PEA	Q84zwl pisum sativ
16	48	49.0	188	Q2ILN7_9DELT	Q2iln7 anaeromyxob
17	48	49.0	298	Q9R587_MOUSE	Q9r587 mus musculu
18	48	49.0	435	Q2JIT0_9CYAN	Q2jito cyanobacter
19	48	49.0	578	1_XKR6_TETNG	Q49lsl tetraodon n
20	48	49.0	578	Q5GH49_FUGRU	Q5gh49 fugu rubrip
21	48	49.0	627	Q74489_SYNY3	P74489 synechocyst
22	47.5	48.5	240	Q97035_HAESO	P97035 haemophilus
23	47.5	48.5	577	Q36XB4_RHOPA	Q36xb4 rhodopseudo
24	47.5	48.5	577	Q37C12_RHOPA	Q37c12 rhodopseudo
25	47.5	48.5	807	Q3VMG0_9CHLB	Q3vmg0 pelodictyon
26	47	48.0	486	Q5U414_XENLA	Q5u414 xenopus lae
27	47	48.0	487	Q32N49_XENLA	Q32n49 xenopus lae
28	47	48.0	910	Q2ZDS6_ORISA	Q2zds6 oryza sativ
29	46	46.9	361	Q2NMB5_SODGL	Q2nmb5 sodalis glo
30	46	46.9	385	Q5ZPA2_9DELT	Q5zpa2 angiococcus
31	46	46.9	540	Q5GH65_MOUSE	Q5gh65 mus musculu

32	46	46.9	580	2	Q5GH40_BRARE	Q5gh40 brachydanio
33	46	46.9	638	1	XKR6_RAT	Q5gh57 rattus norv
34	46	46.9	641	1	XKR6_HUMAN	Q5gh73 homo sapien
35	46	46.9	807	1	SYL_CHLTE	Q8kbv2 chlorobium
36	46	46.9	836	2	Q2Y8V4_NITMU	Q2y8v4 nitrosospir
37	46	46.9	859	2	Q3XW00_9PROT	Q3xw00 magnetococc
38	46	46.9	863	2	Q2S415_9SPHI	Q2s415 salinibacte
39	46	46.9	2484	2	Q5CF27_CRYPV	Q5cf27 cryptospori
40	45	45.9	178	2	Q9RYR0_DEIRA	Q9ryr0 deinococcus
41	45	45.9	219	2	Q6LIT5_PICTO	Q6lit5 microphilus
42	45	45.9	276	2	Q4BS81_BURVI	Q4bs81 burkholderi
43	45	45.9	278	2	Q7VV93_BORPE	Q7vv93 bordetella
44	45	45.9	278	2	Q7W7P3_BORPA	Q7w7p3 bordetella
45	45	45.9	278	2	Q7WL31_BORBR	Q7wl31 bordetella

ALIGNMENTS

RESULT 1
Q3APY5_CHLCH
ID Q3APY5_CHLCH PRELIMINARY; PRT; 805 AA.
AC Q3APY5_CHLCH PRELIMINARY; PRT; 805 AA.
DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 22-NOV-2005, sequence version 1.
DT 21-FEB-2006, entry version 5.
DE Leucyl-tRNA synthetase class Ia (EC 6.1.1.4).
DE OrderedLocusNames=Cag_1688;
GN Chlorobium chlorochromatii (strain Cad3).
OS Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium/Pelodictyon group; Chlorobium.
OX NCBI_TaxID=340177;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barty K., Detter J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Bryant D., Schmutz J., Larimer F.,
RA Land M., Kyrpides N., Ivanova N., Richardson P.;
RT "Complete sequence of Chlorobium chlorochromatii Cad3.";
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
EMBL; CP000108; ABB28940.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0006429; F:leucyl-tRNA aminoacylation; IEA.
KW Aminoacyl-tRNA synthetase; Complete proteome; Ligase.
SQ SEQUENCE 805 AA; 92007 MW; A0C78B83732AF54C CRC64;

Query Match 59.2%; Score 58; DB 2; Length 805;

Best Local Similarity 69.2%; Pred. No. 3.2; Indels 0; Gaps 0;

Matches 9; Conservative 2; Mismatches 2;

Qy 1 GIRRFLGSIWRFI 13

||| ||| : |||:

Db 622 GISRFLGKVRVF 634

RESULT 2

Q25271_LEPDE
ID Q25271_LEPDE PRELIMINARY; PRT; 670 AA.
AC Q25271;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Diapause protein 1 (Fragment).
GN Name=Dp19;
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;

```

DR GO; GO:0015031; P:protein transport; IEA.
DR GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011527; ABC_TM_1.
DR InterPro; IPR001140; ABC_TM_transpt.
DR InterPro; IPR003439; ABC_transp_like.
DR InterPro; IPR005074; Peptidase_C39.
DR InterPro; IPR010132; Type_I_sec_HlyB.
DR PANTHER; PTHR19242:SF74; Type_I_sec_HlyB; 1.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR Pfam; PF03412; Peptidase_C39; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SMO0382; AAA; 1.
DR TIGRFAMS; TIGR01846; type_I_sec_HlyB; 1.
DR PROSITE; PSS0929; ABC_TMIF; 1.
DR PROSITE; PSS0211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PSS0893; ABC_TRANSPORTER_2; 1.
DR PROSITE; PSS0990; PEPTIDASE_C39; 1.
DR PROSITE; PSS0990; PEPTIDASE_C39; 1.
SQ SEQUENCE 735 AA; 80717 MW; 0216259241F3630C CRC64;

Query Match 53.1%; Score 52; DB 2; Length 735;
Best Local Similarity 62.5%; Pred. No. 26;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GIRRFGLSIWRFIRAP 16
   | | | | : | | | : | |
Db 161 GFRWFLPAIWRYRAF 176

RESULT 4
Q44QDI_CHLLI PRELIMINARY; PRT; 805 AA.
AC Q44QDI;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, entry version 1.
DT 21-FEB-2006, entry version 9.
DE Leucyl-tRNA synthetase bacterial/mitochondrial, class Ia.
GN ORFNames=ClimDRAFT_1980;
OS Chlorobium limicola DSM 245.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium/pelodictyon group; Chlorobium.
OX NCBI_TaxID=290315;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 245;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Deter C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RA "Sequencing of the draft genome and assembly of Chlorobium limicola
RT DSM 245.";
RT Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RL [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 245;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Chlorobium limicola
RT 245.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
-----
DR EMBL; AAJ01000009; EAM43320.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
DR GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
DR InterPro; IPR02302; Leu_tRNAasn_1a.
DR Pfam; PF00133; tRNA-synt_1; 1.

```

```
DR PRINTS; PRO0985; TRNASYNTHLEU.
DR TIGRFAMs; TIGR00396; leuS_bact; 1.
KW Aminoacyl-tRNA synthetase.
SQ SEQUENCE 805 AA; 91997 MW; D4F3FE20F9592DF3 CRC64;

Query Match 53.1%; Score 52; DB 2; Length 805;
Best Local Similarity 61.5%; Pred. No. 29;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFI 13
DB 622 GISRFLGKWRV 634

RESULT 5
Q43K01_9CHLB PRELIMINARY; PRT; 816 AA.
ID Q43K01_9CHLB PRELIMINARY; PRT; 816 AA.
AC Q43K01;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, entry version 9.
DE Leucyl-tRNA synthetase bacterial/mitochondrial, class Ia.
GN ORFNames=Cpha266DRAFT_2546;
OS Chlorobium phaeobacteroides DSM 266.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium/Pelodictyon group; Chlorobium.
OX NCBI_TaxID=290317;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 266;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.,
RA "Sequencing of the draft genome and assembly of Chlorobium
RT phaeobacteroides DSM 266."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 266;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.,
RA "Annotation of the draft genome assembly of Chlorobium
RT phaeobacteroides DSM 266."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AAI01000002; EAM35935.1; -; Genomic_DNA.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
DR GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
DR InterPro; IPR002302; Leu_CRNAsyn_1a.
DR Pfam; PF00133; tRNA-synt_1; 1.
DR PRINTS; PRO0985; TRNASYNTHLEU.
DR TIGRFAMs; TIGR00396; leuS_bact; 1.
KW Aminoacyl-tRNA synthetase.
SQ SEQUENCE 816 AA; 93335 MW; 6770B1DAC50560F1 CRC64;

Query Match 53.1%; Score 52; DB 2; Length 816;
Best Local Similarity 61.5%; Pred. No. 29;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFI 13
DB 622 GISRFLGKWRV 634

RESULT 6
Q39L57_BURS3 PRELIMINARY; PRT; 407 AA.
ID Q39L57;
AC Q39L57;
DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, entry version 4.
DE Hypothetical protein.
GN OrderedLocusNames=Bcep18194_A3207;
OS Burkholderia sp. (strain 383) (Burkholderia cepacia (strain ATCC 17760
/ NCIB 9086 / R18194)).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=269483;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Chain P., Malfatti S., Shin M.,
RA Verges L., Schmutz J., Larimer F., Land M., Kyripides N., Lykidis A.,
RA Richardson P.;
RA "Complete sequence of chromosome 1 of Burkholderia sp. 383."
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; CP000151; AB06809.1; -; Genomic_DNA.
DR Complete proteome; Hypothetical protein.
KW SEQUENCE 407 AA; 45483 MW; 957829B27BCABFC1 CRC64;
SQ SEQUENCE 407 AA; 45483 MW; 957829B27BCABFC1 CRC64;

Query Match 52.0%; Score 51; DB 2; Length 407;
Best Local Similarity 47.1%; Pred. No. 20;
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFI 17
DB 327 GIRQMLGHVWQWTRSSV 343

RESULT 7
Q456F4_9BURK PRELIMINARY; PRT; 408 AA.
ID Q456F4_9BURK PRELIMINARY; PRT; 408 AA.
AC Q456F4;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Hypothetical protein.
GN ORFNames=BcenDRAFT_3751;
OS Burkholderia cenocepacia AU 1054.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=331271;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AU 1054;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RA "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT AU 1054."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AU 1054;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT AU 1054."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC
```



```

Query Match      51.0%; Score 50; DB 1; Length 580;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 LGSIRWFIRAFY 17
   ||:|||||
Db 190 LGQWRYLRALY 201

RESULT 13
Q4BFM2_BURVI PRELIMINARY; PRT; 409 AA.
AC Q4BFM2;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Hypothetical protein.
GN ORFNames=Bcep1808DRAFT_3388;
OS Burkholderia vietnamiensis G4.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OC NCB1_TaxID=269482;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G4;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Burkholderia
RT vietnamiensis G4.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G4;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Burkholderia
RT vietnamiensis G4.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
[3]
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G4;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; AAEH0200029; EAM28562.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 409 AA; 45629 MW; CCDJFAS2A9F014E4 CRC64;

Query Match      50.0%; Score 49; DB 2; Length 409;
Best Local Similarity 41.2%; Pred. No. 42;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 GIRFLGSIRWFIRAFY 17
   ||:|||||
Db 329 GVREMLCHVWQWTRSSY 345

RESULT 14
Q3PK79_PARDE PRELIMINARY; PRT; 449 AA.
AC Q3PK79;
DT 25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2005, sequence version 1.

```

```

DT 07-FEB-2006, entry version 4.
DE Cytochrome P450.
GN ORFNames=PdenDRAFT_4722;
OS Paracoccus denitrificans PD1222.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Paracoccus.
OC NCB1_TaxID=318586;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PD1222;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Paracoccus
RT denitrificans PD1222.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PD1222;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Paracoccus denitrificans
RT PD1222.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC -!- SIMILARITY: Balances to the cytochrome P450 family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; AAIT0100001; EAM68115.1; -; Genomic_DNA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0005006; F:iron ion binding; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00463; EP4501.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 449 AA; 50659 MW; 5F3EEC9E12AA3B35 CRC64;

Query Match      50.0%; Score 49; DB 2; Length 449;
Best Local Similarity 64.3%; Pred. No. 46;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 RRFGLSIRWFIRAF 16
   ||:|||||
Db 9 RQGRGSGVWFIRDF 22

RESULT 15
Q84ZW1_PEA PRELIMINARY; PRT; 488 AA.
ID Q84ZW1;
AC Q84ZW1;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Ent-kaurenoic acid oxidase.
GN Name=KA01;
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OC NCB1_TaxID=3888;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Shoot;

```

Tue May 23 08:38:01 2006

RX MEDLINE=22417727; PubMed=12529541; DOI=10.1104/pp.012963;
RA Davidson S.E., Elliott R.C., Helliwell C.A., Poole A.T., Reid J.B.;
RT "The pea gene NA encodes ent-kaurenoic acid oxidase.";
RL Plant Physiol. 131:335-344(2003).
CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum (By
CC similarity).
CC -!- SIMILARITY: Belongs to the cytochrome P450 family.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF37321; AA023063.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR01128; Cytochrome_P450.
DR InterPro; IPR02401; EP450I.
DR PANTHER; PTHR19383; Cytochrome_P450; 1.
DR Pfam; PF00067; P450; 2.
DR PRINTS; PR00463; EP450I.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
DR Endoplasmic reticulum; Heme; Iron; Membrane; Metal-binding;
KW Monooxygenase; Oxidoreductase.
SQ SEQUENCE 488 AA; 56478 MW; 503453CB6E43C830 CRC64;

Query Match 50.0%; Score 49; DB 2; Length 488;
Best Local Similarity 58.3%; Pred.No. 50;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 5 FLGSIMRPIRAF 16
|:|:|:|:|:|:|
Db 54 FIGNWSFLRAF 65

Search completed: May 19, 2006, 14:38:12
Job time : 115.429 secs

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:38:42 ; Search time 24.8571 Seconds
(without alignments)
63.384 Million cell updates/sec

Title: US-10-712-447-2

Perfect score: 98
Sequence: 1 GRRFLGSIWRFIRAFYG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /EMC Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep.*
- 2: /EMC Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep.*
- 3: /EMC Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep.*
- 4: /EMC Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep.*
- 5: /EMC Celerra_SIDS3/ptodata/2/iaa/PCITUS_COMB.pep.*
- 6: /EMC Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep.*
- 7: /EMC Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	79.6	18	2	US-08-940-095-242 Sequence 242, App
2	78	79.6	18	2	US-08-940-093-242 Sequence 242, App
3	78	79.6	18	2	US-08-940-096-242 Sequence 242, App
4	78	79.6	18	2	US-09-465-719-242 Sequence 242, App
5	78	79.6	18	2	US-09-453-605-242 Sequence 242, App
6	78	79.6	18	2	US-09-453-838-242 Sequence 242, App
7	78	79.6	18	2	US-08-940-136-242 Sequence 242, App
8	78	79.6	18	2	US-09-453-841-242 Sequence 242, App
9	78	79.6	18	2	US-09-453-833-242 Sequence 242, App
10	78	79.6	18	2	US-09-453-826-242 Sequence 242, App
11	78	79.6	18	2	US-09-453-840-242 Sequence 242, App
12	78	79.6	18	2	US-09-865-989-242 Sequence 242, App
13	78	79.6	18	2	US-09-453-834-242 Sequence 242, App
14	78	79.6	18	2	US-10-283-599-242 Sequence 242, App
15	78	79.6	18	2	US-09-465-718-242 Sequence 242, App
16	51	52.0	76	2	US-09-205-258-892 Sequence 892, App
17	51	52.0	76	2	US-10-004-860-892 Sequence 892, App
18	47.5	48.5	253	2	US-09-586-106D-49 Sequence 49, App
19	47.5	48.5	253	2	US-10-799-870-49 Sequence 49, App
20	45.5	46.4	254	2	US-09-586-106D-45 Sequence 45, App
21	45.5	46.4	254	2	US-10-799-870-45 Sequence 45, App
22	45	45.9	22	1	US-08-338-882-40 Sequence 40, App
23	45	45.9	22	1	US-08-338-882-41 Sequence 41, App
24	45	45.9	539	2	US-09-710-279-340 Sequence 340, App
25	45	45.9	835	2	US-09-134-001C-5105 Sequence 5105, App
26	45	45.9	877	2	US-09-328-352-8162 Sequence 8162, App

27	44	44.9	22	1	US-08-132-167-50 Sequence 50, Appl
28	44	44.9	589	1	US-08-756-317-5 Sequence 5, Appl
29	44	44.9	1052	2	US-09-134-000C-6620 Sequence 6620, Ap
30	43	43.9	23	2	US-10-360-101-83 Sequence 83, Appl
31	43	43.9	413	3	US-09-609-146-27 Sequence 27, Appl
32	43	43.9	439	3	US-09-609-146-29 Sequence 29, Appl
33	43	43.9	683	2	US-09-902-340-15932 Sequence 15932, A
34	43	43.9	702	2	US-10-094-749-2262 Sequence 2262, Ap
35	43	43.9	812	2	US-09-538-092-643 Sequence 643, Appl
36	42	42.9	14	1	US-08-480-190-3 Sequence 3, Appl
37	42	42.9	14	1	US-08-488-379-3 Sequence 3, Appl
38	42	42.9	14	2	US-08-475-399A-3 Sequence 3, Appl
39	42	42.9	14	2	US-08-077-255A-3 Sequence 3, Appl
40	42	42.9	14	5	PCT-US93-07545-3 Sequence 3, Appl
41	42	42.9	15	1	US-08-480-190-2 Sequence 2, Appl
42	42	42.9	15	1	US-08-488-379-2 Sequence 2, Appl
43	42	42.9	15	2	US-08-475-399A-2 Sequence 2, Appl
44	42	42.9	15	2	US-08-077-255A-2 Sequence 2, Appl
45	42	42.9	15	5	PCT-US93-07545-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-08-940-095-242
; Sequence 242, Application US/08940095
; Patent No. 6004925
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DISLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,095
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6004925e
US-08-940-095-242

Query Match 79.6%; Score 78; DB 2; Length 18;
 Best Local Similarity 72.2%; Pred. No. 1.1e-05;
 Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFVG 18
 ||:|||||:|:|:|
 Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 2

US-08-940-093-242
 ; Sequence 242, Application US/08940093
 ; Patent No. 6037323
 ; GENERAL INFORMATION:
 ; APPLICANT: Dasseux, Jean-Louis
 ; APPLICANT: Sekul, Renate
 ; APPLICANT: Buttner, Klaus
 ; APPLICANT: Cornut, Isabelle
 ; APPLICANT: Metz, Gunther
 ; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
 ; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
 ; NUMBER OF SEQUENCES: 258
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036-2811
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/940,093
 ; FILING DATE: 29-SEP-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 009196-0006-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-493-4935
 ; TELEFAX: 650-493-5556
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 242:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 18 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: No. 6037323e
 ; US-08-940-093-242

Query Match 79.6%; Score 78; DB 2; Length 18;
 Best Local Similarity 72.2%; Pred. No. 1.1e-05;
 Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFVG 18
 ||:|||||:|:|:|
 Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 3

US-08-940-096-242
 ; Sequence 242, Application US/08940096
 ; Patent No. 6046166
 ; GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis
 ; APPLICANT: Sekul, Renate
 ; APPLICANT: Buttner, Klaus
 ; APPLICANT: Cornut, Isabelle
 ; APPLICANT: Metz, Gunther
 ; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
 ; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
 ; NUMBER OF SEQUENCES: 258
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036-2811
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/940,096
 ; FILING DATE: 29-SEP-1997
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 009196-0005-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-493-4935
 ; TELEFAX: 650-493-5556
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 242:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 18 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: No. 6046166e
 ; US-08-940-096-242

Query Match 79.6%; Score 78; DB 2; Length 18;
 Best Local Similarity 72.2%; Pred. No. 1.1e-05;
 Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFVG 18
 ||:|||||:|:~|:|
 Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 4

US-09-465-719-242
 ; Sequence 242, Application US/09465719
 ; Patent No. 6265377
 ; GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis
 ; APPLICANT: Sekul, Renate
 ; APPLICANT: Buttner, Klaus
 ; APPLICANT: Cornut, Isabelle
 ; APPLICANT: Metz, Gunther
 ; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
 ; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
 ; NUMBER OF SEQUENCES: 258
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036-2811

RESULT 3

US-08-940-096-242
 ; Sequence 242, Application US/08940096
 ; Patent No. 6046166
 ; GENERAL INFORMATION:

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/465,719
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,093
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6265377e
US-09-465-719-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFFIRAFVG 18
||:|||||:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 5
US-09-453-605-242
Sequence 242, Application US/09453605
Patent No. 6329341
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
Sekul, Renate
Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,605
FILING DATE: 26-NOV-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6329341e
SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-453-605-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFFIRAFVG 18
||:|||||:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 6
US-09-453-838-242
Sequence 242, Application US/09453838
Patent No. 6376464
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
Sekul, Renate
Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,838
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6376464e

US-09-453-838-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFVG 18
||:|||||:|||||
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 7

US-08-940-136-242
; Sequence 242, Application US/08940136
; Patent No. 6518412
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 29-SEP-1997
; APPLICATION NUMBER: US/08/940,136
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0007-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6518412e

US-08-940-136-242
Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFVG 18
||:|||||:|||||
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 8

US-09-453-841-242
; Sequence 242, Application US/089453833
; Patent No. 6602854
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP

QY 1 GIRRFLGSIWRFIRAFVG 18
||:|||||:|||||
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 9

US-09-453-833-242
; Sequence 242, Application US/09453833
; Patent No. 6602854
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP

QY 1 GIRRFLGSIWRFIRAFVG 18
||:|||||:|||||
Db 1 GIKKFLGSIWKFIKAFVG 18

; Sequence 242, Application US/09453841
; Patent No. 6573239
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,841
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6573239e

US-09-453-841-242
Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFVG 18
||:|||||:|||||
Db 1 GIKKFLGSIWKFIKAFVG 18

```

; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453.833
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6602854e
; US-09-453-833-242

```

```

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

Oy 1 GIRRFLGSIWRFIRAFYG 18
Db 1 GIKKFLGSIWKFIRAFVG 18

```

```

RESULT 10
US-09-453-826-242
; Sequence 242, Application US/09453826
; Patent No. 6630450
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,826
; FILING DATE:
; CLASSIFICATION:

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6630450e
; US-09-453-826-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GIRRFLGSIWRFIRAFYG 18
Db 1 GIKKFLGSIWKFIRAFVG 18

RESULT 11
US-09-453-840-242
; Sequence 242, Application US/09453840
; Patent No. 6716816
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,840
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids

```

```
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6716816e
US-09-453-840-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.le-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 G1RRFLGSIWRFIRAFVG 18
    ||::|||::||::|||
Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 12
US-09-865-989-242
; Sequence 242, Application US/09865989
; Patent No. 6734169
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,989
; FILING DATE: 25-May-2001
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/465,719
; FILING DATE: 17-DEC-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6734169e
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-865-989-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.le-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 G1RRFLGSIWRFIRAFVG 18
    ||::|||::||::|||
Db 1 G1KKFLGSIWKFIKAFVG 18
```

```
RESULT 13
US-09-453-834-242
; Sequence 242, Application US/09453834
; Patent No. 6753313
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,834
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6753313e
US-09-453-834-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.le-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 G1RRFLGSIWRFIRAFVG 18
    ||::|||::||::|||
Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 14
US-10-283-599-242
; Sequence 242, Application US/10283599
; Patent No. 6844327
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
```

TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.

NUMBER OF SEQUENCES: 274

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/283,599

FILING DATE: 29-OCT-2002

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/940,136

FILING DATE: 29-SEP-1997

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009196-0007-999

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 242:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6844327e

US-10-283-599-242

Query Match

Best Local Similarity 79.6%; Score 78; DB 2; Length 18;

Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRKFLGSIWRFIRAFVG 18

Db 1 GIKKFLGSIWKFIRAFVG 18

RESULT 15

US-09-465-718-242

Sequence 242. Application US/09465718

Patent No. 690177

GENERAL INFORMATION:

APPLICANT: Dasseux, Jean-Louis

APPLICANT: Sekul, Renate

APPLICANT: Buttner, Klaus

APPLICANT: Cornut, Isabelle

APPLICANT: Metz, Gunther

TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

NUMBER OF SEQUENCES: 258

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/465,718

FILING DATE: 17-Dec-1999

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/940,096

FILING DATE: 29-SEP-1997

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009196-0005-999

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 242:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6900177e

US-09-465-718-242

Query Match

Best Local Similarity 79.6%; Score 78; DB 2; Length 18;

Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRKFLGSIWRFIRAFVG 18

Db 1 GIKKFLGSIWKFIRAFVG 18

Search completed: May 19, 2006, 14:42:54

Job time : 24.8571 secs

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 15:18:19 ; Search time 81.2857 Seconds
(without alignments)
102.575 Million cell updates/sec

Title: US-10-712-447-2

Perfect score: 98

Sequence: 1 GIRFLGSIWRFIRAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main*

- 1: /EMC Celerra_SIDS3/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
- 2: /EMC Celerra_SIDS3/ptodata/2/pubppaa/US08_PUBCOMB.pep.*
- 3: /EMC Celerra_SIDS3/ptodata/2/pubppaa/US09_PUBCOMB.pep.*
- 4: /EMC Celerra_SIDS3/ptodata/2/pubppaa/US10A_PUBCOMB.pep.*
- 5: /EMC Celerra_SIDS3/ptodata/2/pubppaa/US10B_PUBCOMB.pep.*
- 6: /EMC Celerra_SIDS3/ptodata/2/pubppaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	18	4	US-10-712-447-2
2	98	100.0	18	4	US-10-712-447-5
3	98	100.0	18	4	US-10-712-447-8
4	98	100.0	18	4	US-10-712-447-10
5	98	100.0	18	4	US-10-712-447-13
6	95	96.9	18	4	US-10-712-447-91
7	94	95.9	18	4	US-10-712-447-115
8	94	95.9	18	4	US-10-712-447-116
9	94	95.9	18	4	US-10-712-447-117
10	94	95.9	18	4	US-10-712-447-129
11	94	95.9	18	4	US-10-712-447-131
12	92	93.9	18	4	US-10-712-447-21
13	92	93.9	18	4	US-10-712-447-53
14	92	93.9	18	4	US-10-712-447-74
15	90	91.8	18	4	US-10-712-447-4
16	90	91.8	18	4	US-10-712-447-127
17	89	90.8	18	4	US-10-712-447-99
18	88	89.8	18	4	US-10-712-447-18
19	88	89.8	18	4	US-10-712-447-112
20	88	89.8	18	4	US-10-712-447-113
21	88	89.8	18	4	US-10-712-447-114
22	87	88.8	18	4	US-10-712-447-17
23	86	87.8	18	4	US-10-712-447-61
24	86	87.8	18	4	US-10-712-447-82
25	85	86.7	18	4	US-10-712-447-16
26	85	86.7	18	4	US-10-712-447-96
27	85	86.7	18	4	US-10-712-447-121

Sequence 22, Appl
Sequence 78, Appl
Sequence 95, Appl
Sequence 120, Appl
Sequence 19, Appl
Sequence 56, Appl
Sequence 58, Appl
Sequence 77, Appl
Sequence 79, Appl
Sequence 80, Appl
Sequence 94, Appl
Sequence 57, Appl
Sequence 100, Appl
Sequence 41, Appl
Sequence 97, Appl
Sequence 242, Appl
Sequence 242, Appl

84 85.7 18 4 US-10-712-447-22
84 85.7 18 4 US-10-712-447-78
84 85.7 18 4 US-10-712-447-95
84 85.7 18 4 US-10-712-447-120
82 83.7 18 4 US-10-712-447-19
82 83.7 18 4 US-10-712-447-56
82 83.7 18 4 US-10-712-447-58
82 83.7 18 4 US-10-712-447-77
82 83.7 18 4 US-10-712-447-79
82 83.7 18 4 US-10-712-447-80
82 83.7 18 4 US-10-712-447-94
81 82.7 18 4 US-10-712-447-57
81 82.7 18 4 US-10-712-447-100
80 81.6 18 4 US-10-712-447-41
79 80.6 18 4 US-10-712-447-97
78 79.6 18 3 US-09-865-989-242
78 79.6 18 3 US-09-865-989-242
78 79.6 18 4 US-10-099-574A-242

ALIGNMENTS

RESULT 1

US-10-712-447-2
; Sequence 2, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712.447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; OTHER INFORMATION: c-term amidated
US-10-712-447-2

Query Match 100.0%; Score 98; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 9.8e-08; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

Oy 1 GIRFLGSIWRFIRAFYG 18
|||||

Db 1 GIRFLGSIWRFIRAFYG 18
|||||

RESULT 2

US-10-712-447-5
; Sequence 5, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712.447
; CURRENT FILING DATE: 2003-11-13

```
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-5

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
   |||||
Db 1 GRRFLGSIWRFIRAFYG 18
   |||||

RESULT 3
US-10-712-447-8
; Sequence 8, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-8

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
   |||||
Db 1 GRRFLGSIWRFIRAFYG 18
   |||||

RESULT 4
US-10-712-447-10
; Sequence 10, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 91
; LENGTH: 18

; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-10

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
   |||||
Db 1 GRRFLGSIWRFIRAFYG 18
   |||||

RESULT 5
US-10-712-447-13
; Sequence 13, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-13

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
   |||||
Db 1 GRRFLGSIWRFIRAFYG 18
   |||||

RESULT 6
US-10-712-447-91
; Sequence 91, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 91
; LENGTH: 18
```


Query Match 95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRFLGSIWRFIRAFYG 18
 ||||| : |||
Db 1 GRRFLGSLWRFIRAFYG 18

```

RESULT 11
US-10-712-447-131
; Sequence 131, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 131
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-131

```

Query Match 95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. NO. 3.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 G1RRFLGSIWRF1R1FYG 18
|:|||||:|||||
Db 1 GLRRFLGSIWRF1R1FYG 18

```

RESULT 12
US-10-712-447-21
; Sequence 21, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 21
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-21

```

Query Match 93.9%; Score 92; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 7.9e-07;

Matches	16:	Conservative	2:	Mismatches	0:	Indels	0:	Gaps	0:
---------	-----	--------------	----	------------	----	--------	----	------	----

Qy 1 GIRFLGSIWRFIRAFYG 18
|||:|||||:
Db 1 GIRFELGAIWRFIRSEFYG 18

```

RESULT 13
US-10-712-447-53
; Sequence 53, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARGAR, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 53
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (3)
; OTHER INFORMATION: (Dime)Lys
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (14)
; OTHER INFORMATION: (Dime)Lys
; US-10-712-447-53

```

Query Match 93.9%; Score 92; DB 4; Length 18;
Best Local Similarity 88.9%;
Matches 16: Conservative 2; Mismatches 0; Indels
Pred. No. 7.9e-07;

Qy 1 GIRREFLSIWRFIKAFYG 18
||:|||||:||||
Db 1 GKREFLSIWRFIKAFYG 18

```

RESULT 14
US-10-712-447-74
; Sequence 74, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 74
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

```

OTHER INFORMATION: peptide
US-10-712-447-74
Query Match 93.9%; Score 92; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 7.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18
| | | | | | | | | | | | | | | | | |
Db 1 GIRKFLGSIWRFIRAFYG 18

RESULT 15
US-10-712-447-4
; Sequence 4, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712.447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: Patentin ver. 3.2
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-4

Query Match 91.8%; Score 90; DB 4; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.6e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18
| | | | | | | | | | | | | | | | | |
Db 1 GIRKFLGSIWRFIRAFYG 18

Search completed: May 19, 2006, 15:27:56
Job time : 81.2857 secs

This Page Blank (uspto)

; TITLE OF INVENTION: Methods and Compositions for Treating
 ; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
 ; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
 ; FILE REFERENCE: MPI2001-288P1RCP10NMIM
 ; CURRENT APPLICATION NUMBER: US/11/242.505A
 ; CURRENT FILING DATE: 2005-10-03
 ; PRIOR APPLICATION NUMBER: US 10/290,078
 ; PRIOR FILING DATE: 2002-11-07
 ; PRIOR APPLICATION NUMBER: US 60/347,949
 ; PRIOR FILING DATE: 2001-11-07
 ; PRIOR APPLICATION NUMBER: US 10/320,351
 ; PRIOR FILING DATE: 2002-12-16
 ; PRIOR APPLICATION NUMBER: 60/341,606
 ; PRIOR FILING DATE: 2001-12-17
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 18
 ; LENGTH: 403
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; US-11-242-505A-18

* Query Match 37.8%; Score 37; DB 7; Length 403;
 Best Local Similarity 55.6%; Pred. No. 16;
 * Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 IRRFLGSIW 10
 :|||:|:|:
 Db 155 VRRVLGAV 163

RESULT 3
 US-09-949-925-142
 ; Sequence 142, Application US/09949925
 ; Publication No. US2006009575A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 67 Human secreted proteins
 ; FILE REFERENCE: P2023P2
 ; CURRENT APPLICATION NUMBER: US/09/949,925
 ; CURRENT FILING DATE: 2001-09-12
 ; PRIOR APPLICATION NUMBER: US 60/232,150
 ; PRIOR FILING DATE: 2000-12-09
 ; PRIOR APPLICATION NUMBER: PCT/US99/01621
 ; PRIOR FILING DATE: 1999-01-27
 ; PRIOR APPLICATION NUMBER: US 60/073,160
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,159
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,165
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,164
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,167
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,162
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,161
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,170
 ; PRIOR FILING DATE: 1998-01-30
 ; NUMBER OF SEQ ID NOS: 298
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 142
 ; LENGTH: 60
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (60)
 ; OTHER INFORMATION: Xaa equals stop translation
 US-09-949-925-142

Query Match 37.2%; Score 36.5; DB 1; Length 60;
 Best Local Similarity 57.1%; Pred. No. 2.2;
 Matches 8; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 5 FLGSIWRFIRAFYG 18
 :|||:|:|:
 Db 31 FLILVWIFV-AFYG 43

RESULT 4
 US-09-949-925-111
 ; Sequence 111, Application US/09949925
 ; Publication No. US2006009575A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 67 Human secreted proteins
 ; FILE REFERENCE: P2023P2
 ; CURRENT APPLICATION NUMBER: US/09/949,925
 ; CURRENT FILING DATE: 2001-09-12
 ; PRIOR APPLICATION NUMBER: US 60/232,150
 ; PRIOR FILING DATE: 2000-12-09
 ; PRIOR APPLICATION NUMBER: PCT/US99/01621
 ; PRIOR FILING DATE: 1999-01-27
 ; PRIOR APPLICATION NUMBER: US 60/073,160
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,159
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,165
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,164
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,167
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,162
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,161
 ; PRIOR FILING DATE: 1998-01-30
 ; PRIOR APPLICATION NUMBER: US 60/073,170
 ; PRIOR FILING DATE: 1998-01-30
 ; NUMBER OF SEQ ID NOS: 298
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 111
 ; LENGTH: 74
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (74)
 ; OTHER INFORMATION: Xaa equals stop translation
 US-09-949-925-111

Query Match 36.7%; Score 36; DB 1; Length 74;
 Best Local Similarity 54.5%; Pred. No. 3.3;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IRRFLGSIWRF 12
 :|||:|:|:
 Db 59 LREVSQIWRWF 69

RESULT 5
 US-11-302-678-5
 ; Sequence 5, Application US/11302678
 ; Publication No. US20060088881A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Venkateswarlu, Karicheti
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
 ; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
 ; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
 ; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
 ; FILE REFERENCE: MPI02-012PIRNM_OMNI

; CURRENT APPLICATION NUMBER: US/11/302,678
; CURRENT FILING DATE: 2005-12-14
; PRIOR APPLICATION NUMBER: US/10/345,680
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-302-678-5

Query Match 36.7%; Score 36; DB 7; Length 599;
Best Local Similarity 71.4%; Pred. No. 38;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 LGSWRF 12
DB 64 LGWVWF 70

RESULT 6
US-11-242-505A-48
; Sequence 48, Application US/11242505A
; Publication No. US20060099656A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
; FILE REFERENCE: MPI2001-288PRCPLOMNM
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-242-505A-48

Query Match 34.7%; Score 34; DB 7; Length 313;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 6 LGSWRFIRAFY 17

DB 195 LEEAWSFLDAFY 206

RESULT 7
US-10-511-937-2540
; Sequence 2540, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2540
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2540

Query Match 34.7%; Score 34; DB 6; Length 351;
Best Local Similarity 46.2%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 6 LGSWRFIRAFY 18
DB 263 LGTVLWKLMLFY 275

RESULT 8
US-10-975-692-2
; Sequence 2, Application US/10975692
; Publication No. US20060090221A1
; GENERAL INFORMATION:
; APPLICANT: WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION
; APPLICANT: Browne, John A.
; APPLICANT: Wallis, James G.
; APPLICANT: Watts, Jennifer L.
; TITLE OF INVENTION: DESATURASES AND METHODS OF USING THEM FOR SYNTHESIS OF
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS
; FILE REFERENCE: 4630-58963-02
; CURRENT APPLICATION NUMBER: US/10/975,692
; CURRENT FILING DATE: 2004-10-26
; PRIOR APPLICATION NUMBER: US 09/857,583
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/28655
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/111,301
; PRIOR FILING DATE: 1998-12-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-975-692-2

Query Match 34.7%; Score 34; DB 6; Length 447;
Best Local Similarity 43.8%; Pred. No. 59;
Matches 7; Conservative 4; Mismatches 5; Indels 5; Gaps 0;

QY 2 IRRFLGSIWRFIRAFY 17
||| : : : : :
Db 130 IRKILETIFILFAFY 145

RESULT 9
US-10-505-928-543
; Sequence 543, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 543
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-543

Query Match 34.7%; Score 34; DB 6; Length 522;
Best Local Similarity 47.1%; Pred. No. 70;
Matches 8; Conservative 3; Mismatches 4; Indels 4; Gaps 1;

QY 3 RRFL--GSIWRFIRAFY 17
||| | : : : : :
Db 473 RRFTQSGDLVHRKPH 489

RESULT 10
US-11-169-140-109
; Sequence 109, Application US/11169140
; Publication No. US20060099150A1
; GENERAL INFORMATION:
; APPLICANT: ARIZKE PHARMACEUTICALS, INC.
; APPLICANT: HOUSTON, Lou, L.
; APPLICANT: SHERIDAN, Philip, J.
; APPLICANT: HAWLEY, Stephen
; APPLICANT: GLYNN, Jacqueline, M.
; APPLICANT: CHAPIN, Steven
; TITLE OF INVENTION: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CE
; TITLE OF INVENTION: BARRIERS
; FILE REFERENCE: 11474-037-999
; CURRENT APPLICATION NUMBER: US/11/169,140
; CURRENT FILING DATE: 2005-06-27
; PRIOR APPLICATION NUMBER: US 60/267,601
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/248,819
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/248,478
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 60/237,929
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/949,039
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 09/969,748
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 109
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Simian
US-11-169-140-109

Query Match 34.2%; Score 33.5; DB 7; Length 244;
Best Local Similarity 42.1%; Pred. No. 35;
Matches 8; Conservative 3; Mismatches 3; Indels 5; Gaps 1;

QY 1 GIRRFLGSIW----RPIR 14
| : : : : :
Db 158 GLVLGAVCVARARFIR 176

RESULT 11
US-11-204-427-7
; Sequence 7, Application US/11204427
; Publication No. US20060100146A1
; GENERAL INFORMATION:
; APPLICANT: Sturley, Stephen L
; APPLICANT: Turkish, Aaron R
; APPLICANT: Billheimer, Jeffrey T
; APPLICANT: Cromley, Debra
; TITLE OF INVENTION: AWAT-RELATED METHODS AND ARTICLES
; FILE REFERENCE: 0575/72796/JPM/AJM/JCS
; CURRENT APPLICATION NUMBER: US/11/204,427
; CURRENT FILING DATE: 2005-08-15
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-204-427-7

Query Match 33.7%; Score 33; DB 7; Length 342;
Best Local Similarity 50.8%; Pred. No. 63;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 8 SIWRFIRAFY 17
: ||| : : : :
Db 84 AIWRQLRDYY 93

RESULT 12
US-11-304-129-40
; Sequence 40, Application US/11304129
; Publication No. US20060088915A1
; GENERAL INFORMATION:
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: TAKATSU, Yoshihiro
; APPLICANT: WATANABE, Takuya
; APPLICANT: TERAQ, Yasuko
; APPLICANT: SHINTANI, Yasushi
; APPLICANT: HINUMA, Syuji
; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
; FILE REFERENCE: 2762US0P
; CURRENT APPLICATION NUMBER: US/11/304,129
; CURRENT FILING DATE: 2005-12-15
; PRIOR APPLICATION NUMBER: US/10/333,192
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: JP 2000-217442
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: JP 2001-26779
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/JP01/06162
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 40
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Rat
US-11-304-129-40

Query Match 33.7%; Score 33; DB 7; Length 393;
Best Local Similarity 46.2%; Pred. No. 75;

Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 FLGSIWRIFIRAFY 17

Db 216 FCGIWPVDQOQFY 228

RESULT 13

US-11-304-129-48
; Sequence 48, Application US/11304129
; Publication No. US2006008915A1
; GENERAL INFORMATION:
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: TAKATSU, Yoshihiro
; APPLICANT: WATANABE, Takuya
; APPLICANT: TERAO, Yasuko
; APPLICANT: SHINTANI, Yasushi
; APPLICANT: HINUMA, Syuji
; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
; FILE REFERENCE: 2762USOP
; CURRENT APPLICATION NUMBER: US/11/304,129
; CURRENT FILING DATE: 2005-12-15
; PRIOR APPLICATION NUMBER: US/10/333,192
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: JP 2000-217442
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: JP 2001-26779
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/JP01/06162
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 48
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Mouse
US-11-304-129-48

Query Match 33.7%; Score 33; DB 7; Length 393;

Best Local Similarity 46.2%; Pred. No. 75;

Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 FLGSIWRIFIRAFY 17

Db 216 FCGIWPVDQOQFY 228

RESULT 14

US-10-505-928-545
; Sequence 545, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 545
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-545

Query Match 33.7%; Score 33; DB 6; Length 463;

Best Local Similarity 33.3%; Pred. No. 90;

Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 RFLGSIWRIFIRAFY 18

| : : : |||

Db 339 RYYSSEYHYVGGFYG 353

RESULT 15

US-10-505-928-853
; Sequence 853, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 853
; LENGTH: 1531
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-853

Query Match 33.7%; Score 33; DB 6; Length 1531;

Best Local Similarity 50.0%; Pred. No. 3.6e+02;

Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 LGSIWRFIRAFY 17

Db 1122 LGLIYFFVQRFY 1133

Search completed: May 19, 2006, 15:28:17

Job time : 2.14286 secs

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:13:22 ; Search time 94.2857 Seconds
(without alignments)
87.287 Million cell updates/sec

Title: US-10-712-447-8

Perfect score: 98

Sequence: 1 GRRFLGSIWRFIRAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq_8:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

9: Geneseqp2005s:*

10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	98	100.0	18	8	ADO34231	Ado34231 Synthetic
2	98	100.0	18	8	ADO34225	Ado34225 Synthetic
3	98	100.0	18	8	ADO34228	Ado34228 Synthetic
4	98	100.0	18	8	ADO34236	Ado34236 Synthetic
5	98	100.0	18	8	ADO34233	Ado34233 Synthetic
6	95	96.9	18	8	ADO34314	Ado34314 Synthetic
7	94	95.9	18	8	ADO34354	Ado34354 Synthetic
8	94	95.9	18	8	ADO34338	Ado34338 Synthetic
9	94	95.9	18	8	ADO34352	Ado34352 Synthetic
10	94	95.9	18	8	ADO34340	Ado34340 Synthetic
11	94	95.9	18	8	ADO34339	Ado34339 Synthetic
12	92	93.9	18	8	ADO34297	Ado34297 Synthetic
13	92	93.9	18	8	ADO34244	Ado34244 Synthetic
14	92	93.9	18	8	ADO34276	Ado34276 Synthetic
15	90	91.8	18	8	ADO34227	Ado34227 Synthetic
16	90	91.8	18	8	ADO34350	Ado34350 Synthetic
17	89	90.8	18	8	ADO34322	Ado34322 Synthetic
18	88	89.8	18	8	ADO34336	Ado34336 Synthetic
19	88	89.8	18	8	ADO34335	Ado34335 Synthetic
20	88	89.8	18	8	ADO34337	Ado34337 Synthetic
21	88	89.8	18	8	ADO34241	Ado34241 Synthetic
22	87	88.8	18	8	ADO34240	Ado34240 Synthetic
23	86	87.8	18	8	ADO34284	Ado34284 Synthetic

24	86	87.8	18	8	ADO34305	Ado34305 Synthetic
25	85	86.7	18	8	ADO34239	Ado34239 Synthetic
26	85	86.7	18	8	ADO34344	Ado34344 Synthetic
27	85	86.7	18	8	ADO34319	Ado34319 Synthetic
28	84	85.7	18	8	ADO34245	Ado34245 Synthetic
29	84	85.7	18	8	ADO34301	Ado34301 Synthetic
30	84	85.7	18	8	ADO34343	Ado34343 Synthetic
31	84	85.7	18	8	ADO34318	Ado34318 Synthetic
32	82	83.7	18	8	ADO34302	Ado34302 Synthetic
33	82	83.7	18	8	ADO34279	Ado34279 Synthetic
34	82	83.7	18	8	ADO34303	Ado34303 Synthetic
35	82	83.7	18	8	ADO34242	Ado34242 Synthetic
36	82	83.7	18	8	ADO34300	Ado34300 Synthetic
37	82	83.7	18	8	ADO34281	Ado34281 Synthetic
38	82	83.7	18	8	ADO34317	Ado34317 Synthetic
39	81	82.7	18	8	ADO34323	Ado34323 Synthetic
40	81	82.7	18	8	ADO34280	Ado34280 Synthetic
41	80	81.6	18	8	ADO34264	Ado34264 Synthetic
42	79	80.6	18	8	ADO34320	Ado34320 Synthetic
43	78	79.6	18	2	AA118917	Aay18917 Lecithin:
44	78	79.6	18	2	AA119171	Aay19171 Lecithin:
45	78	79.6	18	2	AA119425	Aay19425 Lecithin:

ALIGNMENTS

RESULT 1

ID ADO34231 standard; peptide; 18 AA.

XX ADO34231;

XX 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 8.

apolipoprotein-E mimicking polypeptide; antilipemic; cardiatic;
vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
atherosclerosis; myocardial infarction; stroke; embolus; angina;
low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

Synthetic.

WO2004043403-A2.

27-MAY-2004.

13-NOV-2003; 2003WO-US036268.

13-NOV-2002; 2002US-0425821P.

(UABR-) UAB RES FOUND.

Anantharamiah GM, Garber DW, Datta G;

WPI; 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

Claim 4; SEQ ID NO 8; 79pp; English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianigmal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;
 Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18
 |||||
 Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 2
 ADO34225
 ID ADO34225 standard; peptide; 18 AA.

AC ADO34225;

XX 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking polypeptide related R18L peptide.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianigmal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 18 /note= "C-terminal amide"

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 2; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,

CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianigmal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18
 |||||
 Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 3
 ADO34228
 ID ADO34228 standard; peptide; 18 AA.

XX ADO34228;

XX 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 5.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianigmal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 5; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject

CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipemic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFYG 18
 |||||
 Db 1 GIRFLGSIWRFIRAFYG 18

RESULT 4
 ADO34236
 ID ADO34236 standard; peptide; 18 AA.

AC ADO34236;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 13.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

PS Claim 4; SEQ ID NO 13; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E

CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipemic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFYG 18
 |||||
 Db 1 GIRFLGSIWRFIRAFYG 18

RESULT 5
 ADO34233
 ID ADO34233 standard; peptide; 18 AA.

AC ADO34233;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 10.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

PS Claim 4; SEQ ID NO 10; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising

CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. NO. 6.4e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18
 |||||
 Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 6

ADO34314
 ID ADO34314 standard; peptide; 18 AA.

XX ADO34314;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 91.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

PN 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 91; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 96.9%; Score 95; DB 8; Length 18;
 Best Local Similarity 94.4%; Pred. NO. 1.8e-07;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18
 |||||
 Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 7

ADO34354

ID ADO34354 standard; peptide; 18 AA.

XX ADO34354;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 131.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

PN 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 131; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;
 SQ

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18
 |:|||||:|||||
 Db 1 GLRRFLGSIWRFIRAFYG 18

RESULT 8

ADO34338
 ID ADO34338 standard; peptide; 18 AA.

XX
 AC ADO34338;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 115.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 115; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18
 |:|||||:|||||
 Db 1 GLRRFLGSIWRFIRAFYG 18

RESULT 9

ADO34352
 ID ADO34352 standard; peptide; 18 AA.

XX
 AC ADO34352;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 129.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 129; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,

CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18
 |||||:||||:|||||
 Db 1 GIRRFLGSLWRFLEAFYG 18

RESULT 10

ADO34340
 ID ADO34340 standard; peptide; 18 AA.

XX
 AC ADO34340;

DT 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 117.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 117; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18

Db 1 GIRRFIGSIWRFLEAFYG 18

RESULT 11

ADO34339

ID ADO34339 standard; peptide; 18 AA.

XX
 AC ADO34339;

XX 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 116.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 116; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;

Best Local Similarity 88.9%; Pred. No. 2.6e-07;

Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18

Db 1 GLRRFIGSIWRFIRAFYG 18

RESULT 12

ADO34297

ID ADO34297 standard; peptide; 18 AA.

XX

AC ADO34297;

XX

DT 12-AUG-2004 (first entry)

XX

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 74.

XX

KW apolipoprotein-E mimicking polypeptide; antilipaeic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX

PN WO2004043403-A2.

XX

PD 27-MAY-2004.

XX

PF 13-NOV-2003; 2003WO-US036268.

XX

PR 13-NOV-2002; 2002US-0425821P.

XX

PA (UABR-) UAB RES FOUND.

XX

PI Anantharamiah GM, Garber DW, Datta G;

XX

PT WPI; 2004-411629/38.

XX

DR Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX

PS Claim 4; SEQ ID NO 74; 79pp; English.

XX

CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal

CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 93.9%; Score 92; DB 8; Length 18;

Best Local Similarity 88.9%; Pred. No. 5.3e-07;

Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18

Db 1 GRRFLGSIWRFIRAFYG 18

RESULT 13

ADO34244

ID ADO34244 standard; peptide; 18 AA.

XX

AC ADO34244;

XX

DT 12-AUG-2004 (first entry)

XX

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 21.

XX

KW apolipoprotein-E mimicking polypeptide; antilipaeic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX

PN WO2004043403-A2.

XX

PD 27-MAY-2004.

XX

PF 13-NOV-2003; 2003WO-US036268.

XX

PR 13-NOV-2002; 2002US-0425821P.

XX

PA (UABR-) UAB RES FOUND.

XX

PI Anantharamiah GM, Garber DW, Datta G;

XX

PT WPI; 2004-411629/38.

XX

DR Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX

PS Claim 4; SEQ ID NO 21; 79pp; English.

XX

CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,

CC chimpanzee or orangutan); for treating coronary artery disease,
CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
CC myocardial infarction or stroke; for breaking an embolus in the subject;
CC and also for treating angina. The synthetic apolipoprotein-E mimicking
CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
CC mimicking polypeptide of the invention.

XX Sequence 18 AA;
SQ

Query Match 93.9%; Score 92; DB 8; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.3e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYFG 18
||:|||||:|||||:|||||
Db 1 GIRRFLGAIWRFIRSFYFG 18

RESULT 14
ADO34276
ID ADO34276 standard; peptide; 18 AA.
XX
AC ADO34276;
XX
DT 12-AUG-2004 (first entry)
XX
DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 53.
XX
KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;
KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1. 18
FT /note= "All Lys residues are DiMethyl-Lysine"
XX
XX WO2004043403-A2.
XX
XX 27-MAY-2004.
XX
XX 13-NOV-2003; 2003WO-US036268.
XX
XX 13-NOV-2002; 2002US-0425821P.
XX
XX (UABR-) UAB RES FOUND.
XX
XX Anantharamiah GM, Garber DW, Datta G;
PI WPI; 2004-411629/38.
XX
XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis
PT comprises an amino acid sequence.
XX
XX Claim 4; SEQ ID NO 53; 79pp; English.
XX
XX The invention relates to a novel synthetic apolipoprotein-E mimicking
CC polypeptide. The invention further comprises an isolated nucleic acid
CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
CC a host cell, a recombinant cell or a transgenic, non-human subject
CC (including animal or plant) comprising the synthetic apolipoprotein-E
CC mimicking polypeptide encoding polynucleotide; a composition comprising
CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
CC an monoclonal antibody that specifically binds to the synthetic
CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
CC mimicking polypeptide has the following activities: antilipaeamic,
CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
CC useful for reducing serum cholesterol in a subject (including a mammal
CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
CC chimpanzee or orangutan); for treating coronary artery disease,
CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
CC myocardial infarction or stroke; for breaking an embolus in the subject;
CC and also for treating angina. The synthetic apolipoprotein-E mimicking
CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
CC mimicking polypeptide of the invention.

XX Sequence 18 AA;
SQ

Query Match 93.9%; Score 92; DB 8; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.3e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYFG 18
||:|||||:|||||:|||||
Db 1 GIRRFLGSIWRFIRAFYFG 18

RESULT 15
ADO34227
ID ADO34227 standard; peptide; 18 AA.
XX
AC ADO34227;
XX
DT 12-AUG-2004 (first entry)
XX
DE Synthetic apolipoprotein-E mimicking related R18L linear peptide.
XX
KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;
KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
XX
OS Synthetic.
XX
XX WO2004043403-A2.
XX
XX 27-MAY-2004.
XX
XX 13-NOV-2003; 2003WO-US036268.
XX
XX 13-NOV-2002; 2002US-0425821P.
XX
XX (UABR-) UAB RES FOUND.
XX
XX Anantharamiah GM, Garber DW, Datta G;
PI WPI; 2004-411629/38.
XX
XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis
PT comprises an amino acid sequence.
XX
XX Claim 4; SEQ ID NO 4; 79pp; English.
XX
XX The invention relates to a novel synthetic apolipoprotein-E mimicking
CC polypeptide. The invention further comprises an isolated nucleic acid
CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
CC a host cell, a recombinant cell or a transgenic, non-human subject
CC (including animal or plant) comprising the synthetic apolipoprotein-E
CC mimicking polypeptide encoding polynucleotide; a composition comprising
CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
CC an monoclonal antibody that specifically binds to the synthetic
CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
CC mimicking polypeptide has the following activities: antilipaeamic,
CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 SQ Sequence 18 AA;

Query Match 91.8%; Score 90; DB 8; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.1e-06;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GRRFLGSIWRFIRAFVG 18
 |||||
 Db 1 GRRFLGSIWRFIRAFVG 18
 |||||

Search completed: May 19, 2006, 14:24:31
 Job time : 94.2857 secs

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:24:57 ; Search time 14.2857 Seconds
(without alignments)
121.233 Million cell updates/sec

Title: US-10-712-447-8

Perfect score: 98

Sequence: 1 GIRFLGSIWRFIRAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*

1: Pirl1.*

2: Pirl2.*

3: Pirl3.*

4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	49.0	627	2 S76462	hypothetical prote
2	45	45.9	178	2 A75578	transcription regu
3	44	44.9	461	1 G64537	2-oxoglutarate/mal
4	44	44.9	589	2 A34341	poly(3-hydroxybuty
5	44	44.9	806	2 A84060	leucyl-tRNA synthet
6	44	44.9	861	2 A84060	leucine-tRNA ligase
7	43.5	44.4	1025	2 A43568	acetylcholinestera
8	43	43.9	265	2 T32316	hypothetical prote
9	43	43.9	489	2 B84733	probable cytochrom
10	43	43.9	516	2 T33269	hypothetical prote
11	43	43.9	812	2 A46417	NIP1 protein - yea
12	43	43.9	1607	2 T04583	reverse transcriptase
13	42.5	43.4	407	2 T32085	penicillin-binding
14	42.5	43.4	760	2 E84953	probable transcrip
15	42	42.9	107	2 T52113	hypothetical prote
16	42	42.9	214	2 D72540	hypothetical prote
17	42	42.9	228	2 T15530	hypothetical prote
18	42	42.9	237	2 B72692	hypothetical prote
19	42	42.9	246	2 I54412	MHC HLA-A cell sur
20	42	42.9	258	2 F71707	o-antigen export s
21	42	42.9	258	2 D97700	o-antigen export s
22	42	42.9	273	1 HLH069	MHC class I histoc
23	42	42.9	365	1 HLH069	MHC class I histoc
24	42	42.9	365	2 I38443	gene HLA-A-0203 pr
25	42	42.9	365	2 I61902	MHC class I histoc
26	42	42.9	365	2 I37542	MHC class I histoc
27	42	42.9	365	2 I84448	MHC class I histoc
28	42	42.9	365	2 I61857	MHC HLA-A2.4a chai
29	42	42.9	365	2 I38442	gene HLA-A-0205 pr

30	42	42.9	537	2 T04745	hypothetical prote
31	42	42.9	803	2 AD1282	leucyl-tRNA synthet
32	42	42.9	803	2 AH1653	leucyl-tRNA synthet
33	42	42.9	804	2 B89961	leucyl-tRNA synthet
34	42	42.9	804	2 D69650	leucine-tRNA ligase
35	41.5	42.3	790	2 T50337	homolog to drosoph
36	41	41.8	131	2 AG2115	hypothetical prote
37	41	41.8	265	2 C42595	rfap protein - Esc
38	41	41.8	279	2 E64109	dimethylsulfoxide
39	41	41.8	359	2 T20575	hypothetical prote
40	41	41.8	364	2 AF2599	hypothetical prote
41	41	41.8	364	2 G97381	probable permease
42	41	41.8	384	2 T08940	hypothetical prote
43	41	41.8	406	2 F96571	hypothetical prote
44	41	41.8	503	2 D96776	hypothetical prote
45	41	41.8	519	1 T02263	cytochrome P450 DW

ALIGNMENTS

RESULT 1

S76462

hypothetical protein - Synecocystis sp. (strain PCC 6803)

C:Species: Synecocystis sp.

A:Variety: PCC 6803

C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: S76462

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis

s.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S76462

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-627 <KAN>

A:Cross-references: UNIPROT:P74489; UNIPARC:UPI00000C103F; EMBL:D90915; GB:AB001339; NID:

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 49.0%; Score 48; DB 2; Length 627;

Best Local Similarity 38.9%; Pred.No. 8.1;

Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFYG 18

Db 597 GLEQLLKKIQLWLRQKFG 614

RESULT 2

A75578

transcription regulator, MarR family - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: A75578

R:White, O.; Eissen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma,

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: A75578

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-178 <WHI>

A:Cross-references: UNIPROT:Q9RYR0; UNIPARC:UPI00000D3BE4; GB:AE001863; GB:AE001825; NID:

A:Experimental source: strain R1

C:Genetics:

A:Gene: DRA0248

A:Map position: 2

Query Match 45.9%; Score 45; DB 2; Length 178;

Best Local Similarity 69.2%; Pred. No. 7.2; Mismatches 0; Indels 4; Gaps 0;

QY 2 IRFLGSIWRFIR 14
| | | | |
Db 23 ILRFLGGIWRNLNR 35

RESULT 3
G64537
2-oxoglutarate/malate translocator - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: G64537
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne-son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodoveky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:9739467; PMID:9252185
A;Accession: G64537
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-461 <TOM>
A;Cross-references: UNIPARC:UPI0000174217; GB:AE000511; TIGR:HP0143
C;Superfamily: 2-oxoglutarate/malate translocator

Query Match 44.9%; Score 44; DB 1; Length 461;
Best Local Similarity 53.8%; Pred. No. 26; Mismatches 2; Indels 4; Gaps 0;

QY 2 IRFLGSIWRFIR 14
: | | | | |
Db 297 VRLLSFWFVR 309

RESULT 4
A34341
poly(3-hydroxybutyrate) synthase (EC 2.3.1.-) - Alcaligenes eutrophus
C;Species: Alcaligenes eutrophus
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C;Accession: A34341; A39190
R;Peoples, O.P.; Sinskey, A.J.
J. Biol. Chem. 264, 15298-15303, 1989
A;Title: Poly-beta-hydroxybutyrate (PHB) biosynthesis in Alcaligenes eutrophus H16. Ident
A;Reference number: A34341; MUID:89359357; PMID:2670936
A;Accession: A34341
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-589 <PEO>
A;Cross-references: UNIPROT:P23608; UNIPARC:UPI0000044953; GB:J05003; NID:g141958; PIDN:
R;Schubert, P.; Krueger, N.; Steinbuechel, A.
J. Bacteriol. 173, 168-175, 1991
A;Title: Molecular analysis of the Alcaligenes eutrophus poly(3-hydroxybutyrate) biosynt
omoter.
A;Reference number: A39190; MUID:91100279; PMID:1987116
A;Accession: A39190
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-219 <SCH>
A;Cross-references: UNIPARC:UPI000016E162; GB:M64341; NID:g141964; PIDN:AAA21979.1; PID:
A;Note: the authors translated the codon TAC for residue 120 as Thr
C;Superfamily: poly(3-hydroxyalkanoic acid) synthase phbC
C;Keywords: acyltransferase

Query Match 44.9%; Score 44; DB 2; Length 589;
Best Local Similarity 47.6%; Pred. No. 33; Mismatches 5; Indels 6; Gaps 1;
Matches 10; Conservative 0

QY 3 RRFLGSIW-----RIFAFY 17
| | | | |

Db 100 RRFAGDAWRTNLNLPYRFAAAFY 120

RESULT 5
A84060
leucyl-tRNA synthetase leuS [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: A84060
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A84060
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-806 <STO>
A;Cross-references: UNIPROT:Q9K788; UNIPARC:UPI0000136555; GB:AP001518; GB:BA000004; NID:
A;Experimental source: strain C-125
C;Genetics:
A;Gene: leuS
C;Superfamily: leucine-tRNA ligase

Query Match 44.9%; Score 44; DB 2; Length 806;
Best Local Similarity 53.8%; Pred. No. 45; Mismatches 2; Indels 4; Gaps 0;
Matches 7; Conservative 0

QY 1 GIRRFLGSIWRFI 13
| | | | |
Db 622 GARRFLDRVWRLL 634

RESULT 6
H64102
leucine-tRNA ligase (EC 6.1.1.4) - Haemophilus influenzae (strain Rd KW20)
N;Alternate names: leucyl-tRNA synthetase
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: H64102
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, L.
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: H64102
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-861 <TIGR>
A;Cross-references: UNIPROT:P43827; UNIPARC:UPI000013655F; GB:U32774; GB:L42023; NID:g15;
C;Genetics:
A;Gene: leuS
C;Superfamily: leucine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 44.9%; Score 44; DB 2; Length 861;
Best Local Similarity 46.2%; Pred. No. 48; Mismatches 3; Indels 4; Gaps 0;
Matches 6; Conservative 0

QY 1 GIRRFLGSIWRFI 13
| | | | |
Db 665 GAKRFLGRVWNLV 677

RESULT 7
AH3568
acriflavin resistance protein F [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AH3568
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova, I.
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesc

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
A;Reference number: AD3252; PMID:11756688
A;Accession: AH3568
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1025 <KUR>
A;Cross-references: UNIPROT:Q8YCQ5; UNIPARC:UPI00000584C8; GB:AE008918; PIDN:AAJ53715.1
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI10473
A;Map position: II
C;Superfamily: hypothetical protein b2075

Query Match 44.4%; Score 43.5; DB 2; Length 1025;
Best Local Similarity 50.0%; Pred. No. 69;
Matches 8; Conservative 4; Mismatches 1; Indels 3; Gaps 1;

QY 5 FLGSIMRFI---RAFY 17
||||| | | | |
Db 531 FLGSVWSFMTLP RSFF 546

RESULT 8
T32316
hypothetical protein F31F4.4 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Dec-2004
C;Accession: T32316
R;Blanchard, M.; Kramer, J.; Elliott, G.; Twyman, B.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of *C. elegans* cosmid F31F4.
A;Reference number: Z21149
A;Accession: T32316
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-265 <BLA>
A;Cross-references: UNIPROT:O17136; UNIPARC:UPI000007D19A; EMBL:AF024503; PIDN:AA870384.
A;Experimental source: strain Bristol N2; clone F31F4
C;Genetics:
A;Gene: CESP:F31F4.4
A;Map position: 5
A;Introns: 13/3; 67/2
C;Superfamily: *Caenorhabditis elegans* hypothetical protein T09F5.1

Query Match 43.9%; Score 43; DB 2; Length 265;
Best Local Similarity 53.8%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 LGSIWRFIRAFY 18
||| | | | |
Db 253 LASLWAFVHAFEG 265

RESULT 9
B84733
Probable cytochrome P450 [imported] - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B84733
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A;Reference number: AB4420; MUID:20083487; PMID:10617197
A;Accession: B84733
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-489 <STO>
A;Cross-references: UNIPROT:Q9ZV72; UNIPARC:UPI000009D8ED; GB:AE002093; NID:G3831452; PI
C;Genetics:
A;Gene: At2g32440

A;Map position: 2
C;Superfamily: *Synechocystis* cytochrome P450 slr0574; cytochrome P450 homology

Query Match 43.9%; Score 43; DB 2; Length 489;
Best Local Similarity 54.5%; Pred. No. 40;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 LGSIWRFIRAF 16
:||| | | | |
Db 54 IGNNWSFLRAF 64

RESULT 10
T33269
hypothetical protein C24B9.13 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33269
R;Murray, J.; Wohlmann, P.; Langston, Y.; O'Neal, D.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of *C. elegans* cosmid C24B9.
A;Reference number: Z21310
A;Accession: T33269
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-516 <MUR>
A;Cross-references: UNIPROT:O76442; UNIPARC:UPI000007D477; EMBL:AF068709; PIDN:AAC19257.1
A;Experimental source: strain Bristol N2; clone C24B9
C;Genetics:
A;Gene: CESP:C24B9.13
A;Map position: 5
A;Introns: 13/3; 67/2; 116/2; 268/2; 315/2; 364/2

Query Match 43.9%; Score 43; DB 2; Length 516;
Best Local Similarity 41.2%; Pred. No. 42;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 IRRFLGSIWRFIRAFY 18
:||| | | | |
Db 252 LKPFITSLMFMHAFDG 268

RESULT 11
A46417
NIP1 protein - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: nuclear import protein; protein YM9924.01c; protein YM9952.11c; protei
C;Species: *Saccharomyces cerevisiae*
C;Date: 21-Sep-1993 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A46417; S53979; S59302
R;Gu, Z.; Moerscheil, R.P.; Sherman, F.; Goldfarb, D.S.
Proc. Natl. Acad. Sci. U.S.A. 89, 10355-10359, 1992
A;Title: NIP1, a gene required for nuclear transport in yeast.
A;Reference number: A46417; MUID:93066237; PMID:1332047
A;Accession: A46417
A;Molecule type: DNA
A;Residues: 1-812 <GUL>
A;Cross-references: UNIPROT:P32497; UNIPARC:UPI000017B2E1; EMBL:I02899
A;Note: sequence extracted from NCBI backbone (NCBIN:117849, NCBIP:117850)
R;Connor, R.; Churcher, C.W.
submitted to the EMBL Data Library, April 1995
A;Reference number: S53969
A;Accession: S53979
A;Molecule type: DNA
A;Residues: 571-592, 'Q', 584-640, 'K', 642, 'K', 644-812 <CON>
A;Cross-references: UNIPARC:UPI0000168ACD; EMBL:Z49212; NID:G798940; PID:G798951; MIPS:Y
R;Churcher, C.W.
submitted to the EMBL Data Library, September 1995
A;Reference number: S59302
A;Accession: S59302
A;Molecule type: DNA
A;Residues: 1-110, 'V', 112-582, 'Q', 584-602 <CHU>
A;Cross-references: UNIPARC:UPI0000168ACA; EMBL:Z54141; NID:G1072408; PID:G984682; MIPS:Y
A;Experimental source: strain AB972

```
C;Genetics:
A;Gene: SGD:NIP1
A;Cross-references: SGD:S0004926; MIPS:YMR309C
A;Map position: 13R

Query Match      43.9%; Score 43; DB 2; Length 812;
Best Local Similarity 53.8%; Pred. No. 66;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 GIRFLGSIWRFI 13
    |::|::|::|:
Db 361 GVKRILGSIFSV 373

RESULT 12
T04583
TMV resistance protein N homolog F23E13.30 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04583; T05507
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Jessee, T.
submitted to the Protein Sequence Database, March 1998
A;Reference number: Z15378
A;Accession: T04583
A;Molecule type: DNA
A;Residues: 1-1607 <BEV>
A;Cross-references: UNIPROT:O65506; UNIPARC:UPI00000AA45C; EMBL:AL022141
A;Experimental source: cultivar Columbia; BAC clone F23E13
R;Bevan, M.; Wedler, H.; Wambutt, R.; Hobeisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schuelke
submitted to the Protein Sequence Database, April 1998
A;Reference number: Z15418
A;Accession: T05507
A;Molecule type: DNA
A;Residues: 1448-1607 <BE2>
A;Cross-references: UNIPARC:UPI000016DBFD; EMBL:AL022373
A;Experimental source: cultivar Columbia; BAC clone T19K4
C;Genetics:
A;Map position: 4
A;Intons: 193/2; 238/2; 556/2; 930/3; 1029/3; 1287/3
A;Note: F23E13.30; T19K4.270

Query Match      43.9%; Score 43; DB 2; Length 1607;
Best Local Similarity 72.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 LGSIRWFIRAF 16
    |||||
Db 1321 LGSRWLRIRGF 1331

RESULT 13
T12085
reverse transcriptase homolog - fava bean (fragment)
C;Species: Vicia faba (fava bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12085
R;Kinoshita, T.; Wada, H.; Masaaki, I.; Shimazaki, K.
submitted to the EMBL Data Library, September 1997
A;Description: Retrotransposon-like cDNAs from guard cell protoplasts in Vicia faba.
A;Reference number: Z17406
A;Accession: T12085
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-407 <KIN>
A;Cross-references: UNIPROT:O22103; UNIPARC:UPI00000AAD3D; EMBL:AB007466; NID:d1170509;
A;Experimental source: guard cell protoplasts
C;Superfamily: pol polyprotein

Query Match      43.4%; Score 42.5; DB 2; Length 407;
Best Local Similarity 57.9%; Pred. No. 40;
Matches 11; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

QY 1 GIRFLGSIW--RFIRAF 16
    ||| ||| : |||||
Db 178 GIRFLGHVGFYRRFIRDF 196

RESULT 14
E84953
penicillin-binding protein 1b [imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C;Accession: E84953
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: E84953
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-760 <STO>
A;Cross-references: UNIPARC:UPI000005E4C8; GB:AP0000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: mrcB; BU200
C;Superfamily: penicillin-binding protein 1B

Query Match      43.4%; Score 42.5; DB 2; Length 760;
Best Local Similarity 44.4%; Pred. No. 74;
Matches 8; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 2 IRRFL-GSIWRFIRAFYG 18
    |||: |||: |||
Db 32 INRFNGKWNFPFTSIYG 49

RESULT 15
T52113
probable transcription co-activator KIWI [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Accession: T52113
R;Cormack, R.S.; Hahlbrock, K.; Somssich, I.E.
Plant J. 14, 685-92, 1998
A;Title: Isolation of putative plant transcriptional coactivators using a modified two-h
A;Reference number: Z25848; MUID:98346011; PMID:9681033
A;Accession: T52113
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-107 <COR>
A;Cross-references: UNIPROT:O65154; UNIPARC:UPI000000C45F; EMBL:AF053302; PIDN:AAC08574.1
A;Experimental source: cultivar Columbia
C;Genetics:
A;Gene: KIWI
A;Map position: V
C;Function:
A;Description: probably plays a role in gene activation during pathogen defence and plant
C;Superfamily: Caenorhabditis elegans hypothetical protein T13F2.2

Query Match      42.9%; Score 42; DB 2; Length 107;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 IRRFLGSIWRFIRAFY 17
    |::|::|::|:
Db 54 VRNNGKIWDIREFY 69

Search completed: May 19, 2006, 14:39:58
Job time : 14.2857 secs
```


GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:13:32 ; Search time 115.429 Seconds
(without alignments)
144.247 Million cell updates/sec

Title: US-10-712-447-8

Perfect score: 98

Sequence: 1 GIRRFLGSIWRFIAPYF 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	59.2	805	2 Q3APY5_CHLCH	Q3ap5 chlorobium
2	54	55.1	670	2 Q25271_LEPDE	Q25271 leptinotars
3	52	53.1	735	2 Q9F7V7_RHILV	Q9f7v7 rhizobium 1
4	52	53.1	805	2 Q44QD1_CHLLI	Q44qd1 chlorobium
5	52	53.1	816	2 Q43K01_CHLBS	Q43k01 chlorobium
6	51	52.0	407	2 Q39L57_BURS3	Q39l57 burkholderi
7	51	52.0	408	2 Q456F4_9BURK	Q456f4 burkholderi
8	51	52.0	408	2 Q4LK44_9BURK	Q4lk44 burkholderi
9	50	51.0	579	1 XKR7_HUMAN	Q5gh72 homo sapien
10	50	51.0	579	1 XKR7_PANTR	Q49le1 pan troglod
11	50	51.0	580	1 XKR7_MOUSE	Q5gh64 mus musculus
12	50	51.0	580	1 XKR7_RAT	Q5gh56 rattus norv
13	49	50.0	409	2 Q4BFM2_BURVI	Q4bfm2 burkholderi
14	49	50.0	449	2 Q3PK79_PARDE	Q3pk79 paracoccus
15	49	50.0	488	2 Q84ZWI_PEA	Q84zwl pisum sativ
16	48	49.0	188	2 Q2ILN7_9DELT	Q2iln7 anaeromyxob
17	48	49.0	298	2 Q8R587_MOUSE	Q8r587 mus musculus
18	48	49.0	435	2 Q2JIT0_9CYAN	Q2jit0 cyanobacter
19	48	49.0	578	1 XKR6_TETNG	Q49l88 tetradodon n
20	48	49.0	578	2 Q5GH49_FUGRU	Q5gh49 fugu rubrip
21	48	49.0	627	2 P74489_SVNY3	P74489 synecocyst
22	47.5	48.5	240	2 P97035_HAESO	P97035 haemophilus
23	47.5	48.5	577	2 Q36X84_RHOPA	Q36xb4 rhodospseudo
24	47.5	48.5	577	2 Q37C12_RHOPA	Q37c12 rhodospseudo
25	47.5	48.5	807	2 Q3VMG0_9CHLB	Q3vmg0 pelodictyon
26	47	48.0	486	2 Q5U414_XENLA	Q5u414 xenopus lae
27	47	48.0	487	2 Q32N49_XENLA	Q32n49 xenopus lae
28	47	48.0	910	2 Q2ZDS6_ORYSA	Q2zds6 oryza sativ
29	46	46.9	361	2 Q2NBS5_SODGL	Q2nbs5 sodalis glo
30	46	46.9	385	2 Q5ZPA2_9DELT	Q5zpa2 angiococcus
31	46	46.9	540	2 Q5GH65_MOUSE	Q5gh65 mus musculus

32 46 46.9 580 2 Q5GH40_BRAHE
33 46 46.9 638 1 XKR6_RAT
34 46 46.9 641 1 XKR6_HUMAN
35 46 46.9 807 1 SYL_CHLTE
36 46 46.9 836 2 Q2Y8V4_NITMU
37 46 46.9 859 2 Q3XW00_MAGETOC
38 46 46.9 863 2 Q2S415_9SPHI
39 46 46.9 2484 2 Q5CP27_CRYPV
40 45 45.9 178 2 Q9RYR0_DEIRA
41 45 45.9 219 2 Q6LIT5_PICTO
42 45 45.9 276 2 Q4BS81_BURVI
43 45 45.9 278 2 Q7VV93_BORPE
44 45 45.9 278 2 Q7W7P3_BORPA
45 45 45.9 278 2 Q7WL31_BORBR

ALIGNMENTS

RESULT 1
Q3APY5_CHLCH
ID Q3APY5_CHLCH PRELIMINARY; PRT; 805 AA.
AC Q3APY5_2005, integrated into UniProtKB/TrEMBL.
DT 22-NOV-2005, sequence version 1.
DT 21-FEB-2006, entry version 5.
DE Leucyl-tRNA synthetase class Ia (EC 6.1.1.4).
GN OrderedLocusNames=Cag.1688;
OS Chlorobium chlorochromatii (strain Cad3).
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium/Felodictyon group; Chlorobium.
OX NCBI_TaxID=340177;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Bryant D., Schmutz J., Larimer F.,
RA Land M., Kyrpides N., Ivanova N., Richardson P.,
RA "Complete sequence of Chlorobium chlorochromatii Cad3.";
RT Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
RL -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; CP000108; ABB28940.1; -; Genomic_DNA.
DR GO; GO:0005324; F:ATP binding; IEA.
DR GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
KW Aminoacyl-tRNA synthetase; Complete proteome; Ligase.
SQ SEQUENCE 805 AA; 92007 MW; A0C78B83732AF54C CRC64;

Query Match 59.2%; Score 58; DB 2; Length 805;

Best Local Similarity 69.2%; Pred. No. 3.2; Indels 0; Gaps 0;

Matches 9; Conservative 2; Mismatches 2;

Qy 1 GIRRFLGSIWRFI 13

||| ||| ||| |||

Db 622 GISRFLGKVRFEV 634

RESULT 2

Q25271_LEPDE
ID Q25271_LEPDE PRELIMINARY; PRT; 670 AA.
AC Q25271_1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Diapause protein 1 (Fragment).
GN Name=Dp19;
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;

```

GO; GO:0015031; P:protein transport; IEA.
GO; GO:0006508; P:proteolysis; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011527; ABC_TM_1.
DR InterPro; IPR001140; ABC_TM_transp.
DR InterPro; IPR003439; ABC_transep.
DR InterPro; IPR005074; Peptidase_C39.
DR InterPro; IPR010132; Type_I_sec_HlyB.
DR PANTHER; PTHR13242:SF74; Type_I_sec_HlyB; 1.
DR Pfam; PF00664; ABC_membrane; 1.
DR Pfam; PF00005; ABC_tran; 1.
DR Pfam; PF03412; Peptidase_C39; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRFRAMES; TIGR01846; type_I_sec_HlyB; 1.
DR PROSITE; PS0929; ABC_TMIIF; 1.
DR PROSITE; PS0211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS0893; ABC_TRANSPORTER_2; 1.
DR PROSITE; PS0990; PEPTIDASE_C39; 1.
SQ SEQUENCE 735 AA; 80717 MW; 0216259241F3630C CRC64;

Query Match          53.1%; Score 52; DB 2; Length 735;
Best Local Similarity 62.5%; Pred. No. 26;
Matches 10; Conservative      2; Mismatches    4; Indels      0; Gaps      0;

QY      1 GIRRFGLSGIWRFTRAF 16
        ||||| :|||: |||
DB      161 GFRWFLPAIWRYRRAF 176

RESULT 4
Q44QD1 CHLLI
ID Q44QD1 CHLLI PRELIMINARY; PRT; 805 AA.
AC Q44QD1;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 21-SEP-2005, sequence version 1.
DT 21-FEB-2006, entry version 9.
DE Leucyl-tRNA synthetase bacterial/mitochondrial, class Ia.
GN ORFNames=ClimDRAFT_1980;
OS Chlorobium limicola DSM 245.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium/Pelodictyon group; Chlorobium.
ON NCBI_TaxID=290315;
RX [1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=DSM 245;
RC US DOE Joint Genome Institute (JGI-PGF);
RG Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pieluck S., Richardson P.;
RA "Sequencing of the draft genome and assembly of Chlorobium limicola
RT DSM 245.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=DSM 245;
RC US DOE Joint Genome Institute (JGI-ORNL);
RG Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Chlorobium limicola DSM
RT 245.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
-----
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
-----
CC EMBL; AAHQJ01000009; EAM43320.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
DR GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
DR InterPro; IPR002302; Leu_tRNAsyn_Ia.
DR Pfam; PF00133; tRNA-synt_1; 1.

```

```

DR PRINTS; PRO0985; TRNASYNTHLEU.
KW TIGRFAMs; TIGR00396; leus_bact; 1.
SQ SEQUENCE 805 AA; 91997 MW; D4F3FE28F9B92DF3 CRC64;

Query Match 53.1%; Score 52; DB 2; Length 805;
Best Local Similarity 61.5%; Pred. No. 29;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFI 13
Db 622 GISRFLGKWRVLV 634

RESULT 5
Q43K01_9CHLB PRELIMINARY; PRT; 816 AA.
ID Q43K01_9CHLB PRELIMINARY; PRT; 816 AA.
AC Q43K01;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, entry version 9.
DE Leucyl-tRNA synthetase bacterial/mitochondrial, class Ia.
GN ORFNames=Cpha266DRAFT_2546;
OS Chlorobium phaeobacteroides DSM 266.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium/pelodictyon group; Chlorobium.
OX NCBI_TaxID=290317;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 266;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.,
RT "Sequencing of the draft genome and assembly of Chlorobium
RT phaeobacteroides DSM 266.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 266;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.,
RA "Annotation of the draft genome assembly of Chlorobium
RT phaeobacteroides DSM 266.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AAI01000002; EMB35935.1; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
DR GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
DR InterPro; IPR002302; Leu tRNAasn_1a.
DR Pfam; PF00133; tRNA-synt_1_1.
DR PRINTS; PR00985; TRNASYNTHLEU.
DR TIGRFAMs; TIGR00396; leus_bact; 1.
KW Aminoacyl-tRNA synthetase.
SQ SEQUENCE 816 AA; 93335 MW; 6770B1DAC50560F1 CRC64;

Query Match 53.1%; Score 52; DB 2; Length 816;
Best Local Similarity 61.5%; Pred. No. 29;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFI 13
Db 622 GISRFLGKWRVLV 634

RESULT 6
Q39L57_BURS3 PRELIMINARY; PRT; 407 AA.
ID Q39L57;
AC Q39L57;
DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, entry version 4.
DE Hypothetical protein.
GN OrderedLocNames=Bcep18194_A3207;
OS Burkholderia sp. (strain 383) (Burkholderia cepacia (strain ATCC 17760
OS / NCIB 9086 / R18194)).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=269483;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Chain P., Malfatti S., Shin M.,
RA Vergez L., Schmutz J., Larimer F., Land M., Kyrpides N., Lykidis A.,
RA Richardson P.;
RT "Complete sequence of chromosome 1 of Burkholderia sp. 383.";
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; CP000151; AB06809.1; Genomic_DNA.
DR Complete proteome; Hypothetical protein.
KW SEQUENCE 407 AA; 45483 MW; 957829B27BCABFC1 CRC64;
SQ SEQUENCE 407 AA; 45483 MW; 957829B27BCABFC1 CRC64;

Query Match 52.0%; Score 51; DB 2; Length 407;
Best Local Similarity 47.1%; Pred. No. 20;
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFI 17
Db 327 GIRQLGHVQWTRSSY 343

RESULT 7
Q456F4_9BURK PRELIMINARY; PRT; 408 AA.
ID Q456F4_9BURK PRELIMINARY; PRT; 408 AA.
AC Q456F4;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Hypothetical protein.
GN ORFNames=BcendRAFT_3751;
OS Burkholderia cenocepacia AU 1054.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=331271;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AU 1054;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT AU 1054.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AU 1054;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT AU 1054.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms

```

Name=XKR7; Synonyms=C20orf159, XRG7;
 Homo sapiens (Human).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mamalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 Homo.
 NCBI_TaxID=9606;
 [1]
 NUCLEOTIDE SEQUENCE [MRNA].
 Huang C.-H., Chen Y.;
 "A superfamily of XK-related genes (XRG) widely expressed in
 vertebrates and invertebrates."
 Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 [2]
 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414868a;
 Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
 Jones M., Stavridis G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 Coulson A., Coville G.J., Deadman R., Dhami P., Dunn M.,
 Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 Hammond S., Hawley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 Leharstaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 Marsh V.L., Martin S.L., McConachie L.J., McLeay J.C., Nickerson T.,
 Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,
 Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 Stuke C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 Tracey A., Tromans A.C., Vaudin M., Wall M.L., Wallis J.M.,
 Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 Rogers J.;
 "The DNA sequence and comparative analysis of human chromosome 20.";
 Nature 414:865-871(2001).
 -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
 (potential).
 -1- SIMILARITY: Belongs to the XK family.
 -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous
 gene model prediction.

 Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 Distributed under the Creative Commons Attribution-NoDerivs License

 ENBL; AY534245; AAT07094.1; -; mRNA.
 ENBL; AL031658; CAB88102.1; ALT SEQ; Genomic_DNA.
 Ensembl; ENSG00000101321; Homo sapiens.
 HGNC; HGNC:23062; XKR7.
 Membrane; Transmembrane.
 CHAIN 1 579
 XK-related protein 7.
 /FTID=PRO_0000190788.
 TRANSMEM 59 79
 Potential.
 TRANSMEM 89 109
 Potential.
 TRANSMEM 260 280
 Potential.
 TRANSMEM 314 334
 Potential.
 TRANSMEM 355 375
 Potential.
 TRANSMEM 384 404
 Potential.
 TRANSMEM 415 435
 Potential.
 SEQUENCE 579 AA; 63826 MW; D8D0FF64B9EDD53D CRC64;
 Query Match 51.0%; Score 50; DB 1; Length 579;
 Best Local Similarity 58.3%; Pred. No. 42;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0
 6 LGSIRFIRAFY 17
 |||:|||||
 |||:|||||

```
Db      190 LGQVWRYLRALY 201

RESULT 10
XKR7 PANTR          STANDARD;          PRT;    579 AA.
AC Q49LS1;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE XK-related protein 7.
GN Name=XKR7; Synonyms=XRG7;
OS Pan troglodytes (Hominidae).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pan.
OX NCBI_TaxID=9598;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Huang C.-H., Chen Y.;
RT "A superfamily of XK-related genes (XRG) widely expressed in
RT vertebrates and invertebrates.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -!- SIMILARITY: Belongs to the XK family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY702910; AAV83783.1; -; mRNA.
KW Membrane; Transmembrane.
FT CHAIN 1 579
FT TRANSMEM 59 79
FT TRANSMEM 89 109
FT TRANSMEM 260 280
FT TRANSMEM 314 334
FT TRANSMEM 355 375
FT TRANSMEM 384 404
FT TRANSMEM 415 435
SQ SEQUENCE 579 AA; 63593 MW; 6DFE1191093B85D4 CRC64;

Query Match 51.0%; Score 50; DB 1; Length 579;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 LGSWRFIRAFY 17
||:|||||
Db      190 LGQVWRYLRALY 201

RESULT 11
XKR7 MOUSE          STANDARD;          PRT;    580 AA.
AC Q5GH64;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE XK-related protein 7.
GN Name=Xkr7; Synonyms=Xrg7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=C57BL/6J;
RA Huang C.-H., Chen Y.;
RT "A superfamily of XK-related genes (XRG) widely expressed in
RT vertebrates and invertebrates.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

Query Match 51.0%; Score 50; DB 1; Length 579;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 LGSWRFIRAFY 17
||:|||||
Db      190 LGQVWRYLRALY 201

RESULT 12
XKR7 RAT            STANDARD;          PRT;    580 AA.
ID -XKR7 RAT
AC Q5GH56;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE XK-related protein 7.
GN Name=Xkr7; Synonyms=Xrg7;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Sprague-Dawley;
RA Huang C.-H., Chen Y.;
RT "A superfamily of XK-related genes (XRG) widely expressed in
RT vertebrates and invertebrates.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -!- SIMILARITY: Belongs to the XK family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY534261; AAT07110.1; -; mRNA.
KW Membrane; Transmembrane.
FT CHAIN 1 580
FT TRANSMEM 59 79
FT TRANSMEM 89 109
FT TRANSMEM 260 280
FT TRANSMEM 303 323
FT TRANSMEM 326 346
FT TRANSMEM 355 375
FT TRANSMEM 384 404
FT TRANSMEM 415 435
SQ SEQUENCE 580 AA; 64302 MW; F3291FABF4C5A826 CRC64;

Query Match 51.0%; Score 50; DB 1; Length 580;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 LGSWRFIRAFY 17
||:|||||
Db      190 LGQVWRYLRALY 201
```

```
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -!- SIMILARITY: Belongs to the XK family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY534253; AAT07102.1; -; mRNA.
DR Ensembl; ENSMUSG0000042631; Mus musculus.
DR MGI; MGI:3526711; Xkr7.
KW Membrane; Transmembrane.
FT CHAIN 1 580
FT TRANSMEM 59 79
FT TRANSMEM 89 109
FT TRANSMEM 260 280
FT TRANSMEM 303 323
FT TRANSMEM 326 346
FT TRANSMEM 355 375
FT TRANSMEM 384 404
FT TRANSMEM 415 435
SQ SEQUENCE 580 AA; 64302 MW; F3291FABF4C5A826 CRC64;

Query Match 51.0%; Score 50; DB 1; Length 580;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 LGSWRFIRAFY 17
||:|||||
Db      190 LGQVWRYLRALY 201

RESULT 12
XKR7 RAT            STANDARD;          PRT;    580 AA.
ID -XKR7 RAT
AC Q5GH56;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE XK-related protein 7.
GN Name=Xkr7; Synonyms=Xrg7;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Sprague-Dawley;
RA Huang C.-H., Chen Y.;
RT "A superfamily of XK-related genes (XRG) widely expressed in
RT vertebrates and invertebrates.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -!- SIMILARITY: Belongs to the XK family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY534261; AAT07110.1; -; mRNA.
KW Membrane; Transmembrane.
FT CHAIN 1 580
FT TRANSMEM 59 79
FT TRANSMEM 89 109
FT TRANSMEM 260 280
FT TRANSMEM 303 323
FT TRANSMEM 326 346
FT TRANSMEM 355 375
FT TRANSMEM 384 404
FT TRANSMEM 415 435
SQ SEQUENCE 580 AA; 64338 MW; 8F4907F391B4F5BE CRC64;
```

Query Match 51.0%; Score 50; DB 1; Length 580;
 Best Local Similarity 58.3%; Pred. No. 42;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 LGSIRWFIRAFY 17
 ||:|||||
 DB 190 LGQWRYLRALY 201

RESULT 13

Q4BFM2_BURVI PRELIMINARY; PRT; 409 AA.

AC Q4BFM2; integrated into UniProtKB/TrEMBL.

DT 13-SEP-2005, sequence version 1.

DT 07-FEB-2006, entry version 2.

DE Hypothetical protein.

GN ORFNames=Bcep1808DRAFT_3388;

OS Burkholderia vietnamiensis G4.

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.

OX NCBI_TaxID=269482;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=G4;

RG US DOE Joint Genome Institute (JGI-PGF);

RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,

RA Hammon N., Israni S., Pitluck S., Richardson P.,

RT "Sequencing of the draft genome and assembly of Burkholderia

RT vietnamiensis G4";

RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=G4;

RG US DOE Joint Genome Institute (JGI-ORNL);

RA Larimer F., Land M.,

RT "Annotation of the draft genome assembly of Burkholderia vietnamiensis

RT G4";

RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.

RN [3]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=G4;

RG US DOE Joint Genome Institute (JGI-PGF);

RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,

RA Hammon N., Israni S., Pitluck S., Richardson P.,

RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.

-1- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

CC -----

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>

CC Distributed under the Creative Commons Attribution-NoDerivs License

CC -----

DR EMBL; AAHE0200029; EAM28562.1; -; Genomic_DNA.

XW Hypothetical protein.

SQ SEQUENCE 409 AA; 45629 MW; CCD3FA52A9F014E4 CRC64;

Query Match 50.0%; Score 49; DB 2; Length 409;

Best Local Similarity 41.2%; Pred. No. 42;

Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 GINRFLGSIWRFIRAFY 17

||:|||||

DB 329 GVREMLGHVWQWTRSSY 345

RESULT 14

Q3PK79_PARDE PRELIMINARY; PRT; 449 AA.

AC Q3PK79; integrated into UniProtKB/TrEMBL.

DT 25-OCT-2005, sequence version 1.

DT 25-OCT-2005, sequence version 1.

DT 07-FEB-2006, entry version 4.
 DE Cytochrome P450.
 GN ORFNames=PdenDRAFT_4722;
 OS Paracoccus denitrificans PD1222.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
 OC Rhodobacteraceae; Paracoccus.
 OX NCBI_TaxID=318586;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PD1222;
 RG US DOE Joint Genome Institute (JGI-PGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
 RA Hammon N., Israni S., Pitluck S., Richardson P.,
 RT "Sequencing of the draft genome and assembly of Paracoccus
 RT denitrificans PD1222";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PD1222;
 RG US DOE Joint Genome Institute (JGI-ORNL);
 RA Larimer F., Land M.,
 RT "Annotation of the draft genome assembly of Paracoccus denitrificans
 RT PD1222";
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
 CC -----

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>

CC Distributed under the Creative Commons Attribution-NoDerivs License

CC -----

DR EMBL; AAIT01000001; EAM68115.1; -; Genomic_DNA.

DR GO; GO:0020037; F:heme binding; IEA.

DR GO; GO:0005506; F:iron ion binding; IEA.

DR GO; GO:0046872; F:metal ion binding; IEA.

DR GO; GO:0004497; F:monooxygenase activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR001128; Cytochrome_P450.

DR Pfam; PF00067; P450; 1.

DR PRINTS; PR00463; EP4501.

DR PRINTS; PR00385; P450.

DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.

KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase.

SQ SEQUENCE 449 AA; 50659 MW; 5F3EEC9E12AA3B35 CRC64;

Query Match 50.0%; Score 49; DB 2; Length 449;

Best Local Similarity 64.3%; Pred. No. 46;

Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 RRFLGSIWRFIRAF 16

||:|||||

DB 9 RQGRGSIWRFIRDF 22

RESULT 15

Q84ZW1_PEA

PRELIMINARY; PRT; 488 AA.

AC Q84ZW1;

DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.

DT 01-JUN-2003, sequence version 1.

DT 07-FEB-2006, entry version 21.

DE Ent-kaurenoic acid oxidase.

GN Name=KAO1;

OS Pisum sativum (Garden pea).

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

OC Rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.

OX NCBI_TaxID=3888;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RT TISSUE=Shoot;

Search completed: May 19, 2006, 14:38:14
Job time : 115.429 secs

is Page Blank (uspto)


```
Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.le-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFGLSIWRFIRAFVG 18
   ||:|||||:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 2
US-08-940-093-242
; Sequence 242, Application US/08940093
; Patent No. 6037323
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,093
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6037323e
; US-08-940-093-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.le-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFGLSIWRFIRAFVG 18
   ||:|||||:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 3
US-08-940-096-242
; Sequence 242, Application US/08940096
; Patent No. 6046166
; GENERAL INFORMATION:
```

```
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,096
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6046166e
; US-08-940-096-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.le-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFGLSIWRFIRAFVG 18
   ||:|||||:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 4
US-09-465-719-242
; Sequence 242, Application US/09465719
; Patent No. 6265377
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
```

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/465,719
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,093
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6265377e
; US-09-465-719-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFFIRAFVG 18
||:|||||:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 5
US-09-453-605-242
; Sequence 242, Application US/09453605
; Patent No. 6329341
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,605
; FILING DATE: 26-NOV. 6329341-1999
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
```

```
;
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6329341e
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:
; US-09-453-605-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFFIRAFVG 18
||:|||||:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 6
US-09-453-838-242
; Sequence 242, Application US/09453838
; Patent No. 6376464
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,838
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6376464e
```

```
US-09-453-838-242
Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 G1RRFLGSIWRRFIRAFVG 18
   ||:|||||:|:|:|
Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 7
US-08-940-136-242
; Sequence 242, Application US/08940136
; Patent No. 6518412
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; TITLE OF INVENTION: SUPPLY APOLOPOPROTEIN A-I AGONISTS AND THEIR
; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 29-SEP-1997
; APPLICATION NUMBER: US/08/940,136
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0007-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6518412e
US-08-940-136-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 G1RRFLGSIWRRFIRAFVG 18
   ||:|||||:|:|:|
Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 8
US-09-453-841-242
; Sequence 242, Application US/09453841
; Patent No. 6573239
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLOPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,841
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6573239e
US-09-453-841-242

Query Match          79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 G1RRFLGSIWRRFIRAFYG 18
   ||:|||||:|:|:|
Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 9
US-09-453-833-242
; Sequence 242, Application US/09453833
; Patent No. 6602854
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLOPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
```

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453.833
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: linear
MOLECULE TYPE: No. 6602854e
US-09-453-833-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFVG 18
||:|||||:|:|
Db 1 GIKKFLGSIWKFIRAFVG 18

RESULT 10
US-09-453-826-242
Sequence 242, Application US/09453826
Patent No. 6630450
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453.826
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6630450e
US-09-453-826-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFVG 18
||:|||||:|:|
Db 1 GIKKFLGSIWKFIRAFVG 18

RESULT 11
US-09-453-840-242
Sequence 242, Application US/09453840
Patent No. 6716816
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,840
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids

```
;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6716816e
US-09-453-840-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 G1RRFLGSIWRFIRAFYG 18
Db 1 G1KKFLGSIWKF1KAFVG 18

RESULT 12
US-09-865-989-242
; Sequence 242, Application US/09865989
; Patent No. 6734169
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,989
; FILING DATE: 25-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/465,719
; FILING DATE: 17-DEC-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6734169e
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-865-989-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 G1RRFLGSIWRFIRAFYG 18
Db 1 G1KKFLGSIWKF1KAFVG 18

RESULT 13
US-09-453-834-242
; Sequence 242, Application US/09453834
; Patent No. 6753313
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,834
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6753313e
; US-09-453-834-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 G1RRFLGSIWRFIRAFYG 18
Db 1 G1KKFLGSIWKF1KAFVG 18

RESULT 14
US-10-283-599-242
; Sequence 242, Application US/10283599
; Patent No. 6844327
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
```

;; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
;; NUMBER OF SEQUENCES: 274
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds LLP
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: NY
;; COUNTRY: USA
;; ZIP: 10036-2811
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSEQ Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/283,599
;; FILING DATE: 29-OCT-2002
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/940,136
;; FILING DATE: 29-SEP-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coruzzi, Laura A
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 009196-0007-999
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-493-4935
;; TELEFAX: 650-493-5556
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 242:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: No. 6844327e
;; US-10-283-599-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GIRRFLGSIWRFIRAFYG 18
||:|||||:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 15

US-09-465-718-242
;; Sequence 242, Application US/09465718
;; Patent No. 6900177
;; GENERAL INFORMATION:
;; APPLICANT: Dasseux, Jean-Louis
;; APPLICANT: Sekul, Renate
;; APPLICANT: Buttner, Klaus
;; APPLICANT: Cornut, Isabelle
;; APPLICANT: Metz, Gunther
;; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
;; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;; NUMBER OF SEQUENCES: 258
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds LLP
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: NY
;; COUNTRY: USA
;; ZIP: 10036-2811
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSEQ Version 2.0
;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/465,718
;; FILING DATE: 17-Dec-1999
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/940,096
;; FILING DATE: 29-SEP-1997
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coruzzi, Laura A
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 009196-0005-999
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-493-4935
;; TELEFAX: 650-493-5556
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 242:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: No. 6900177e
;; US-09-465-718-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GIRRFLGSIWRFIRAFYG 18
||:|||||:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

Search completed: May 19, 2006, 14:42:55
Job time : 24.8571 secs

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 15:18:19 ; Search time 81.2857 Seconds
(without alignments)
102.575 Million cell updates/sec

Title: US-10-712-447-8

Perfect score: 98

Sequence: 1 GIRFLGSIWRFIRAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	18	4	US-10-712-447-2
2	98	100.0	18	4	US-10-712-447-5
3	98	100.0	18	4	US-10-712-447-8
4	98	100.0	18	4	US-10-712-447-10
5	98	100.0	18	4	US-10-712-447-13
6	95	96.9	18	4	US-10-712-447-91
7	94	95.9	18	4	US-10-712-447-115
8	94	95.9	18	4	US-10-712-447-116
9	94	95.9	18	4	US-10-712-447-117
10	94	95.9	18	4	US-10-712-447-129
11	94	95.9	18	4	US-10-712-447-131
12	92	93.9	18	4	US-10-712-447-21
13	92	93.9	18	4	US-10-712-447-53
14	92	93.9	18	4	US-10-712-447-74
15	90	91.8	18	4	US-10-712-447-4
16	90	91.8	18	4	US-10-712-447-127
17	89	90.8	18	4	US-10-712-447-99
18	88	89.8	18	4	US-10-712-447-18
19	88	89.8	18	4	US-10-712-447-112
20	88	89.8	18	4	US-10-712-447-113
21	88	89.8	18	4	US-10-712-447-114
22	87	88.8	18	4	US-10-712-447-17
23	86	87.8	18	4	US-10-712-447-61
24	86	87.8	18	4	US-10-712-447-82
25	85	86.7	18	4	US-10-712-447-16
26	85	86.7	18	4	US-10-712-447-96
27	85	86.7	18	4	US-10-712-447-121

28 84 85.7 18 4 US-10-712-447-22 Sequence 22, Appl
29 84 85.7 18 4 US-10-712-447-78 Sequence 78, Appl
30 84 85.7 18 4 US-10-712-447-95 Sequence 95, Appl
31 84 85.7 18 4 US-10-712-447-120 Sequence 120, Appl
32 82 83.7 18 4 US-10-712-447-19 Sequence 19, Appl
33 82 83.7 18 4 US-10-712-447-56 Sequence 56, Appl
34 82 83.7 18 4 US-10-712-447-58 Sequence 58, Appl
35 82 83.7 18 4 US-10-712-447-77 Sequence 77, Appl
36 82 83.7 18 4 US-10-712-447-79 Sequence 79, Appl
37 82 83.7 18 4 US-10-712-447-80 Sequence 80, Appl
38 82 83.7 18 4 US-10-712-447-94 Sequence 94, Appl
39 81 82.7 18 4 US-10-712-447-57 Sequence 57, Appl
40 81 82.7 18 4 US-10-712-447-100 Sequence 100, Appl
41 80 81.6 18 4 US-10-712-447-41 Sequence 41, Appl
42 79 80.6 18 4 US-10-712-447-97 Sequence 97, Appl
43 78 79.6 18 3 US-09-865-989-242 Sequence 242, Appl
44 78 79.6 18 3 US-09-865-989-242 Sequence 242, Appl
45 78 79.6 18 4 US-10-099-574A-242 Sequence 242, Appl

ALIGNMENTS

RESULT 1
US-10-712-447-2
; Sequence 2, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GABER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; OTHER INFORMATION: c-term amidated
US-10-712-447-2

Query Match 100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

Qy 1 GIRFLGSIWRFIRAFYG 18
|||||
Db 1 GIRFLGSIWRFIRAFYG 18
|||||

RESULT 2
US-10-712-447-5
; Sequence 5, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GABER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13

```
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-5

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFRFYG 18
Db 1 GRRFLGSIWRFRFYG 18

RESULT 3
US-10-712-447-8
; Sequence 8, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-8

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFRFYG 18
Db 1 GRRFLGSIWRFRFYG 18

RESULT 4
US-10-712-447-10
; Sequence 10, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 91
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-10

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFRFYG 18
Db 1 GRRFLGSIWRFRFYG 18

RESULT 5
US-10-712-447-13
; Sequence 13, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-13

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFRFYG 18
Db 1 GRRFLGSIWRFRFYG 18

RESULT 6
US-10-712-447-91
; Sequence 91, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 91
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-91

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFRFYG 18
Db 1 GRRFLGSIWRFRFYG 18
```


Tue May 23 08:38:01 2006

OTHER INFORMATION: peptide
US-10-712-447-74

Query Match 93.9%; Score 92; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 7.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRREFLSIWRIFAFYG 18
|||:|||||||:||||
Db 1 GIRREFLSIWRIFAFYG 18

RESULT 15

US-10-712-447-4
; Sequence 4, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-4

Query Match 91.8%; Score 90; DB 4; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.6e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRREFLSIWRIFAFYG 18
|||:|||||||:||||
Db 1 GIRREFLSIWRIFAFVG 18

Search completed: May 19, 2006, 15:27:57
Job time : 81.2857 secs

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 15:18:37 ; Search time 2.14286 Seconds
(without alignments)
17.943 Million cell updates/sec

Title: US-10-712-447-8

Perfect score: 98

Sequence: 1 GRRFLGSIWRFIRAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications_AA_New:
- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pap.*
 - 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pap.*
 - 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pap.*
 - 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pap.*
 - 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pap.*
 - 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pap.*
 - 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pap.*
 - 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37.5	38.3	441	6	US-10-511-937-2947
2	37	37.8	403	7	US-11-242-505A-18
3	36.5	37.2	60	1	US-09-949-925-142
4	36	36.7	74	1	US-09-949-925-111
5	36	36.7	599	7	US-11-302-678-5
6	34	34.7	313	7	US-11-242-505A-48
7	34	34.7	351	6	US-10-511-937-2540
8	34	34.7	447	6	US-10-975-692-2
9	34	34.7	522	6	US-10-505-928-543
10	33.5	34.2	244	7	US-11-169-140-109
11	33	33.7	342	7	US-11-204-427-7
12	33	33.7	393	7	US-11-304-129-40
13	33	33.7	393	7	US-11-304-129-48
14	33	33.7	463	6	US-10-505-928-545
15	33	33.7	1531	6	US-10-505-928-853
16	33	33.7	1534	6	US-10-505-928-40
17	33	33.7	2202	6	US-10-488-015-12
18	32	32.7	364	7	US-11-113-081A-6
19	32	32.7	388	6	US-10-196-749-336
20	32	32.7	388	7	US-11-024-544A-169
21	32	32.7	388	7	US-11-190-750-137
22	32	32.7	388	7	US-11-204-427-1
23	32	32.7	544	6	US-10-196-749-274
24	32	32.7	581	7	US-11-251-465-18
25	32	32.7	747	7	US-11-261-384-2

26	32	32.7	764	7	US-11-223-738-6	Sequence 6, Appli
27	32	32.7	1503	7	US-11-312-958-48	Sequence 48, Appli
28	31.5	32.1	503	7	US-11-024-544A-21	Sequence 21, Appli
29	31.5	32.1	503	7	US-11-190-750-135	Sequence 135, App
30	31.5	32.1	503	7	US-11-264-784-87	Sequence 87, Appli
31	31	31.6	126	7	US-11-075-891-23	Sequence 23, Appli
32	31	31.6	258	6	US-10-541-993-26	Sequence 26, Appli
33	31	31.6	561	6	US-10-505-928-163	Sequence 163, App
34	31	31.6	643	6	US-10-504-120-19	Sequence 19, Appli
35	31	31.6	651	6	US-10-511-937-2401	Sequence 2401, Ap
36	31	31.6	667	7	US-11-311-555-16	Sequence 16, Appli
37	31	31.6	667	7	US-11-311-561-16	Sequence 16, Appli
38	31	31.6	714	6	US-10-868-498-2	Sequence 2, Appli
39	31	31.6	749	6	US-10-505-928-443	Sequence 443, App
40	31	31.6	919	7	US-11-302-678-62	Sequence 62, Appli
41	30.5	31.1	222	7	US-11-257-062-44	Sequence 44, Appli
42	30	30.6	269	6	US-10-511-455-19	Sequence 19, Appli
43	30	30.6	282	7	US-11-251-466-46	Sequence 46, Appli
44	30	30.6	282	7	US-11-264-784-72	Sequence 72, Appli
45	30	30.6	308	6	US-10-511-455-23	Sequence 23, Appli

ALIGNMENTS

RESULT 1
US-10-511-937-2947
; Sequence 2947, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2947
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2947

Query Match 38.3%; Score 37.5; DB 6; Length 441;
Best Local Similarity 33.3%; Pred. No. 15;
Matches 7; Conservative 5; Mismatches 6; Indels 3; Gaps 1;

Qy 1 GRRFLGSIW---RFRIRAFYG 18
|:|||||:|:
Db 106 GLSKFLGTHLMGNILRLFLG 126

RESULT 2
US-11-242-505A-18
; Sequence 18, Application US/11242505A
; Publication No. US20060099656A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen

```
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
; FILE REFERENCE: MPI2001-288P1RCPL0NMNM
; CURRENT APPLICATION NUMBER: US/11/242.505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-11-242-505A-18

Query Match      37.8%; Score 37; DB 7; Length 403;
Best Local Similarity 55.6%; Pred. No. 16;
Matches 5; Conservative 3; Mismatches 1; Indels 1; Gaps 0;

QY      2 IRRFLGSIW 10
      :|||:||:|
Db      155 VRRVLGAVW 163

RESULT 3
US-09-949-925-142
; Sequence 142, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 142
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (60)
; OTHER INFORMATION: Xaa equals stop translation
US-09-949-925-142
```

```
Query Match      37.2%; Score 36.5; DB 1; Length 60;
Best Local Similarity 57.1%; Pred. No. 2.2;
Matches 8; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY      5 FLGSIWRFIAPYV 18
      :|||:||:|
Db      31 FLILVWIFV-APYV 43

RESULT 4
US-09-949-925-111
; Sequence 111, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (74)
; OTHER INFORMATION: Xaa equals stop translation
US-09-949-925-111

Query Match      36.7%; Score 36; DB 1; Length 74;
Best Local Similarity 54.5%; Pred. No. 3.3;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2 IRRFLGSIWR 12
      :|||:||:|
Db      59 LREVSGKIWR 69

RESULT 5
US-11-302-678-5
; Sequence 5, Application US/11302678
; Publication No. US2006008881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 5089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MPI02-012PIRNM_OMNI
```


; CURRENT APPLICATION NUMBER: US/11/302,678
; CURRENT FILING DATE: 2005-12-14
; PRIOR APPLICATION NUMBER: US/10/345,680
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-302-678-5

Query Match 36.7%; Score 36; DB 7; Length 599;
Best Local Similarity 71.4%; Pred. No. 38;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LGSWRF 12
Db 64 LGSWRF 70

RESULT 6
US-11-242-505A-48
; Sequence 48, Application US/11242505A
; Publication No. US2006009656A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
; FILE REFERENCE: MPI2001-288PLRCPIOMNIM
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-242-505A-48

Query Match 34.7%; Score 34; DB 7; Length 313;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 6 LGSWRF 17

Db 195 LEEAWFLDAFY 206

RESULT 7
US-10-511-937-2540
; Sequence 2540, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2540
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2540

Query Match 34.7%; Score 34; DB 6; Length 351;
Best Local Similarity 46.2%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 6 LGSWRFIRAFY 18
Db 263 LGTVLKEMLFY 275

RESULT 8
US-10-975-692-2
; Sequence 2, Application US/10975692
; Publication No. US20060090221A1
; GENERAL INFORMATION:
; APPLICANT: WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION
; APPLICANT: Browne, John A
; APPLICANT: Wallis, James G
; APPLICANT: Watts, Jennifer L.
; TITLE OF INVENTION: DESATURASES AND METHODS OF USING THEM FOR SYNTHESIS OF
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS
; FILE REFERENCE: 4630-58963-02
; CURRENT APPLICATION NUMBER: US/10/975,692
; CURRENT FILING DATE: 2004-10-26
; PRIOR APPLICATION NUMBER: US 09/857,583
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/28655
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/111,301
; PRIOR FILING DATE: 1998-12-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-975-692-2

Query Match 34.7%; Score 34; DB 6; Length 447;
Best Local Similarity 43.8%; Pred. No. 59;
Matches 7; Conservative 4; Mismatches 5; Indels 5; Gaps 0;

QY 2 IRRFGLSGIRAFY 17
Db 130 IRKLEITILFAFY 145
||:|:|:|:|:|:|

RESULT 9
US-10-505-928-543
; Sequence 543, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 543
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-543

Query Match 34.7%; Score 34; DB 6; Length 522;
Best Local Similarity 47.1%; Pred. No. 70;
Matches 8; Conservative 3; Mismatches 4; Indels 4; Gaps 1;

QY 3 RREF--GSIWRFIRAFY 17
Db 473 RRFQSGDLYHRKHF 489
||| | : : | : |

RESULT 10
US-11-169-140-109
; Sequence 109, Application US/11169140
; Publication No. US20060099150A1
; GENERAL INFORMATION:
; APPLICANT: ARIZEXE PHARMACEUTICALS, INC.
; APPLICANT: HOUSTON, Lou, L.
; APPLICANT: SHERIDAN, Philip, J.
; APPLICANT: HAWLEY, Stephen
; APPLICANT: GLYNN, Jacqueline, M.
; APPLICANT: CHAPIN, Steven
; TITLE OF INVENTION: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CE
; TITLE OF INVENTION: BARRIERS
; FILE REFERENCE: 11474-037-999
; CURRENT APPLICATION NUMBER: US/11/169,140
; CURRENT FILING DATE: 2005-06-27
; PRIOR APPLICATION NUMBER: US 60/267,601
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/248,819
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/248,478
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 60/237,929
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/949,039
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 09/969,748
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 109
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Simian
US-11-169-140-109

Query Match 34.2%; Score 33.5; DB 7; Length 244;
Best Local Similarity 42.1%; Pred. No. 35;
Matches 8; Conservative 3; Mismatches 3; Indels 5; Gaps 1;

QY 1 GRRFLGSIW----RFR 14
Db 158 GLVLGAVWCVARAFIR 176
|:|:|:|:|:|

RESULT 11
US-11-204-427-7
; Sequence 7, Application US/11204427
; Publication No. US20060100146A1
; GENERAL INFORMATION:
; APPLICANT: Sturley, Stephen L
; APPLICANT: Turkish, Aaron R
; APPLICANT: Billheimer, Jeffrey T
; APPLICANT: Cromley, Debra
; TITLE OF INVENTION: AWAT-RELATED METHODS AND ARTICLES
; FILE REFERENCE: 0575/72796/JPM/AJM/JCS
; CURRENT APPLICATION NUMBER: US/11/204,427
; CURRENT FILING DATE: 2005-08-15
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-204-427-7

Query Match 33.7%; Score 33; DB 7; Length 342;
Best Local Similarity 50.0%; Pred. No. 63;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 8 SIWRFIRAFY 17
Db 84 AIWRQLRDY 93
:|:|:|:|:|

RESULT 12
US-11-304-129-40
; Sequence 40, Application US/11304129
; Publication No. US20060088915A1
; GENERAL INFORMATION:
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: TAKATSU, Yoshihiro
; APPLICANT: WATANABE, Takuya
; APPLICANT: TERAQ, Yasuko
; APPLICANT: SHINTANI, Yasushi
; APPLICANT: HINUMA, Syuji
; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
; FILE REFERENCE: 2762USOP
; CURRENT APPLICATION NUMBER: US/11/304,129
; CURRENT FILING DATE: 2005-12-15
; PRIOR APPLICATION NUMBER: US/10/333,192
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: JP 2000-217442
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: JP 2001-26779
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/JP01/06162
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 40
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Rat
US-11-304-129-40

Query Match 33.7%; Score 33; DB 7; Length 393;
Best Local Similarity 46.2%; Pred. No. 75;

```
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 FLGSIWRFIRAFY 17
Db 216 FCGIWPVDQQFY 228

RESULT 13
US-11-304-129-48
; Sequence 48, Application US/11304129
; Publication No. US2006008915A1
; GENERAL INFORMATION:
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: TAKATSU, Yoshihiro
; APPLICANT: WATANABE, Takuya
; APPLICANT: TERAOKA, Yasuko
; APPLICANT: SHINTANI, Yasushi
; APPLICANT: HINUMA, Syuji
; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
; FILE REFERENCE: 2762USOP
; CURRENT APPLICATION NUMBER: US/11/304,129
; CURRENT FILING DATE: 2005-12-15
; PRIOR APPLICATION NUMBER: US/10/333,192
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: JP 2000-217442
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: JP 2001-26779
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/JP01/06162
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 48
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Mouse
US-11-304-129-48

Query Match 33.7%; Score 33; DB 7; Length 393;
Best Local Similarity 46.2%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 FLGSIWRFIRAFY 17
Db 216 FCGIWPVDQQFY 228

RESULT 14
US-10-505-928-545
; Sequence 545, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 545
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-545

Query Match 33.7%; Score 33; DB 6; Length 463;
Best Local Similarity 33.3%; Pred. No. 90;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 4 RFLGSIWRFIRAFY 18
| : : : |
```

```
Db 339 RYYSSEYHYVGGPYG 353

RESULT 15
US-10-505-928-853
; Sequence 853, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 853
; LENGTH: 1531
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-853

Query Match 33.7%; Score 33; DB 6; Length 1531;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 LGSIWRFIRAFY 17
| : : : |
Db 1122 LGLIYFVQRFY 1133

Search completed: May 19, 2006, 15:28:18
Job time : 2.14286 secs
```

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:13:22 ; Search time 94.2857 Seconds
(without alignments)
87.287 Million cell updates/sec

Title: US-10-712-447-10

Perfect score: 98

Sequence: 1 GRRFLGSIWRFIRAFYX 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_8:

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB	ID	Description
1	98	100.0	18	8	ADO34231	ADO34231	Synthetic
2	98	100.0	18	8	ADO34225	ADO34225	Synthetic
3	98	100.0	18	8	ADO34228	ADO34228	Synthetic
4	98	100.0	18	8	ADO34236	ADO34236	Synthetic
5	98	100.0	18	8	ADO34233	ADO34233	Synthetic
6	95	96.9	18	8	ADO34314	ADO34314	Synthetic
7	94	95.9	18	8	ADO34354	ADO34354	Synthetic
8	94	95.9	18	8	ADO34338	ADO34338	Synthetic
9	94	95.9	18	8	ADO34352	ADO34352	Synthetic
10	94	95.9	18	8	ADO34340	ADO34340	Synthetic
11	94	95.9	18	8	ADO34339	ADO34339	Synthetic
12	92	93.9	18	8	ADO34297	ADO34297	Synthetic
13	92	93.9	18	8	ADO34244	ADO34244	Synthetic
14	92	93.9	18	8	ADO34276	ADO34276	Synthetic
15	90	91.8	18	8	ADO34227	ADO34227	Synthetic
16	90	91.8	18	8	ADO34350	ADO34350	Synthetic
17	89	90.8	18	8	ADO34322	ADO34322	Synthetic
18	88	89.8	18	8	ADO34336	ADO34336	Synthetic
19	88	89.8	18	8	ADO34335	ADO34335	Synthetic
20	88	89.8	18	8	ADO34337	ADO34337	Synthetic
21	88	89.8	18	8	ADO34241	ADO34241	Synthetic
22	87	88.8	18	8	ADO34240	ADO34240	Synthetic
23	86	87.8	18	8	ADO34284	ADO34284	Synthetic

24	86	87.8	18	8	ADO34305	ADO34305	Synthetic
25	85	86.7	18	8	ADO34239	ADO34239	Synthetic
26	85	86.7	18	8	ADO34344	ADO34344	Synthetic
27	85	86.7	18	8	ADO34319	ADO34319	Synthetic
28	84	85.7	18	8	ADO34245	ADO34245	Synthetic
29	84	85.7	18	8	ADO34301	ADO34301	Synthetic
30	84	85.7	18	8	ADO34343	ADO34343	Synthetic
31	84	85.7	18	8	ADO34318	ADO34318	Synthetic
32	82	83.7	18	8	ADO34302	ADO34302	Synthetic
33	82	83.7	18	8	ADO34279	ADO34279	Synthetic
34	82	83.7	18	8	ADO34303	ADO34303	Synthetic
35	82	83.7	18	8	ADO34242	ADO34242	Synthetic
36	82	83.7	18	8	ADO34300	ADO34300	Synthetic
37	82	83.7	18	8	ADO34281	ADO34281	Synthetic
38	82	83.7	18	8	ADO34317	ADO34317	Synthetic
39	81	82.7	18	8	ADO34323	ADO34323	Synthetic
40	81	82.7	18	8	ADO34280	ADO34280	Synthetic
41	80	81.6	18	8	ADO34264	ADO34264	Synthetic
42	79	80.6	18	8	ADO34320	ADO34320	Synthetic
43	78	79.6	18	2	AA18917	AA18917	Lecithin:
44	78	79.6	18	2	AA19171	AA19171	Lecithin:
45	78	79.6	18	2	AA19425	AA19425	Lecithin:

ALIGNMENTS

RESULT 1

ID ADO34231 standard; peptide; 18 AA.

XX ADO34231;

XX 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 8.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiac;
KW vasotrophic; antiarteriosclerotic; cerebroprotective; antianginal;
KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 8; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
CC polypeptide. The invention further comprises an isolated nucleic acid
CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
CC a host cell, a recombinant cell or a transgenic, non-human subject
CC (including animal or plant) comprising the synthetic apolipoprotein-E
CC mimicking polypeptide encoding polynucleotide; a composition comprising
CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
CC an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;
 SQ Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRIFAFYG 18
 Db 1 GIRFLGSIWRIFAFYG 18
 |||||

RESULT 2
 ADO34225
 ID ADO34225 standard; peptide; 18 AA.

XX AC ADO34225;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking polypeptide related R18L peptide.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 18 /note= "C-terminal amide"

XX WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 2; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,

CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRIFAFYG 18
 Db 1 GIRFLGSIWRIFAFYG 18
 |||||

RESULT 3
 ADO34228
 ID ADO34228 standard; peptide; 18 AA.

XX AC ADO34228;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 5.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 5; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,

CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipemic,
 CC cardiatic, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18

Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 4

ADO34236

ID ADO34236 standard; peptide; 18 AA.

XX AC ADO34236;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 13.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiatic;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX FN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

PS Claim 4; SEQ ID NO 13; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E

CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipemic,
 CC cardiatic, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18

Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 5

ADO34233

ID ADO34233 standard; peptide; 18 AA.

XX AC ADO34233;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 10.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiatic;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX FN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

PS Claim 4; SEQ ID NO 10; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising

CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic, and
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 XX SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRIFAFYVG 18
 |||:|||||
 Db 1 GIRRFLGSIWRIFAFYVG 18

RESULT 6
 ADO34314
 ID ADO34314 standard; peptide; 18 AA.
 XX
 AC ADO34314;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 91.
 XX
 KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
 XX
 OS Synthetic.
 XX
 PN WO2004043403-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 13-NOV-2003; 2003WO-US036268.
 XX
 PR 13-NOV-2002; 2002US-0425821P.
 XX
 PA (UABR-) UAB RES FOUND.
 XX
 PI Anantharamiah GM, Garber DW, Datta G;
 XX
 DR WPI; 2004-411629/38.
 XX
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.
 XX
 PS Claim 4; SEQ ID NO 91; 79pp; English.
 XX
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic, and
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 XX SQ Sequence 18 AA;

Query Match 96.9%; Score 95; DB 8; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.8e-07;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRIFAFYVG 18
 |||:|||||
 Db 1 GIRRFLGSIWRIFAFYVG 18

RESULT 7
 ADO34354
 ID ADO34354 standard; peptide; 18 AA.
 XX
 AC ADO34354;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 131.
 XX
 KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
 XX
 OS Synthetic.
 XX
 PN WO2004043403-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 13-NOV-2003; 2003WO-US036268.
 XX
 PR 13-NOV-2002; 2002US-0425821P.
 XX
 PA (UABR-) UAB RES FOUND.
 XX
 PI Anantharamiah GM, Garber DW, Datta G;
 XX
 DR WPI; 2004-411629/38.
 XX
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.
 XX
 PS Claim 4; SEQ ID NO 131; 79pp; English.
 XX
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRFLGSIWRFIRAFYG 18

Db 1 GLRRFLGSIWRFIRAFYG 18

RESULT 8
 ADO34338
 ID ADO34338 standard; peptide; 18 AA.

XX

AC ADO34338;

XX

DT 12-AUG-2004 (first entry)

XX

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 115.

XX

KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX

PN WO2004043403-A2.

XX

PD 27-MAY-2004.

XX

PF 13-NOV-2003; 2003WO-US036268.

XX

PR 13-NOV-2002; 2002US-0425821P.

XX

PA (UABR-) UAB RES FOUND.

XX

PI Anantharamiah GM, Garber DW, Datta G;

XX

DR WPI; 2004-411629/38.

XX

PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX

PS Claim 4; SEQ ID NO 115; 79pp; English.

XX

CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRFLGSIWRFIRAFYG 18

Db 1 GLRRFLGSIWRFIRAFYG 18

RESULT 9

ADO34352
 ID ADO34352 standard; peptide; 18 AA.

XX

AC ADO34352;

XX

DT 12-AUG-2004 (first entry)

XX

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 129.

XX

KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX

PN WO2004043403-A2.

XX

PD 27-MAY-2004.

XX

PF 13-NOV-2003; 2003WO-US036268.

XX

PR 13-NOV-2002; 2002US-0425821P.

XX

PA (UABR-) UAB RES FOUND.

XX

PI Anantharamiah GM, Garber DW, Datta G;

XX

DR WPI; 2004-411629/38.

XX

PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX

PS Claim 4; SEQ ID NO 129; 79pp; English.

XX

CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,

CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antiangiinal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFIRAFYVG 18
 |||||:||||:||||
 Db 1 GIRRFGLSLWRFIRAFYVG 18

RESULT 10

ADO34340 ADO34340 standard; peptide; 18 AA.

XX AC ADO34340;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 117.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antiangiinal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 117; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

CC antiangiinal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFIRAFYVG 18
 |||||:||||:||||
 Db 1 GIRRFGLSLWRFIRAFYVG 18

RESULT 11

ADO34339

ID ADO34339 standard; peptide; 18 AA.

XX AC ADO34339;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 116.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antiangiinal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 116; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antiangiinal. The synthetic apolipoprotein-E mimicking polypeptide is

Query Match 93.9%; Score 92; DB 8; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.3e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 G1RREFLGS1WRF1RAFYG 18
|||:|||||:||||
Db 1 G1RKFLGS1WRF1KAIFYG 18

RESULT 13
ADO34244
ID ADO34244 standard: peptide: 18 AA:

XX

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 21.

KW apolipoprotein-E mimicking polypeptide; antilipemic; cardiatic;
 KW vasotropic; antiatherosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

WO2004043403-A2

27-MAY-2004.

13-NOV-2003: 2003WO-US036268.

PR 13-NOV-2002: 2002US-0425821P.

PA (UABR-) UAB RES FOUND.

PI Anantharamiah GM, Garber DW, Datta G;

WPI: 2004-411629/38.

Synthetic apolipoprotein-E mimicking polypeptide useful for treating coronary artery disease, dysbetalipoproteinemia or atherosclerosis comprises an amino acid sequence.

PS Claim 4: SEO ID NO 21: 79pp: English.

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, including a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipemic, cardiatic, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,

CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 93.9%; Score 92; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 5.3e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRFLGSIWRFIRAFYVG 18
 ||:|||||:|||||:|||||
 Db 1 GIRFLGAIWRFIRSFYVG 18

RESULT 14
 ADO34276

ID ADO34276 standard; peptide; 18 AA.

AC ADO34276;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 53.

KW apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
 XX Synthetic.

OS Synthetic.

FH Key Location/Qualifiers

FT Modified-site 1. 18

XX /note= "All Lys residues are DiMethyl-Lysine"

PN WO2004043403-A2.

XX 27-MAY-2004.

PF 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

PA Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating

PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis

XX comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 53; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipemic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 93.9%; Score 92; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 5.3e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRFLGSIWRFIRAFYVG 18

||:|||||:|||||:|||||
 Db 1 GIRFLGSIWRFIRAFYVG 18

RESULT 15

ADO34227

ID ADO34227 standard; peptide; 18 AA.

AC ADO34227;

XX 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking related R18L linear peptide.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein, VLDL.

OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

PA Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 XX comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 4; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipemic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

CC useful for reducing serum cholesterol in a subject (including a mammal
CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
CC chimpanzee or orangutan); for treating coronary artery disease,
CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
CC myocardial infarction or stroke; for breaking an embolus in the subject;
CC and also for treating angina. The synthetic apolipoprotein-E mimicking
CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
CC mimicking polypeptide of the invention.

XX
SQ Sequence 18 AA;

Query Match 91.8%; Score 90; DB 8; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.1e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GIRRFLGSIWRFIRAFVG 18
| | | | | | | | | | | | | | | | | |
Db 1 GIRRFLGSIWRFIRAFVG 18

Search completed: May 19, 2006, 14:24:31
Job time : 94.2857 secs

This Page Blank (uspio)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:24:57 ; Search time 14.2857 Seconds
(without alignments)
121.233 Million cell updates/sec

Title: US-10-712-447-10
Perfect score: 98
Sequence: 1 GIRRFLGSIWRFIRAFYG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	49.0	627	2	S76462
2	45	45.9	178	2	A75578
3	44	44.9	461	1	G54537
4	44	44.9	589	2	A34341
5	44	44.9	806	2	A84060
6	44	44.9	861	2	H64102
7	43.5	44.4	1025	2	AH3568
8	43	43.9	265	2	T32316
9	43	43.9	489	2	B84733
10	43	43.9	516	2	T33269
11	43	43.9	812	2	A46417
12	43	43.9	1607	2	T04583
13	42.5	43.4	407	2	T12085
14	42.5	43.4	760	2	E84953
15	42	42.9	107	2	T52113
16	42	42.9	214	2	D72540
17	42	42.9	228	2	T15530
18	42	42.9	237	2	B72692
19	42	42.9	246	2	I54412
20	42	42.9	258	2	D71707
21	42	42.9	258	2	D97700
22	42	42.9	273	1	HLHU69
23	42	42.9	365	1	HLHUA2
24	42	42.9	365	2	I38443
25	42	42.9	365	2	I61902
26	42	42.9	365	2	I37542
27	42	42.9	365	2	I84448
28	42	42.9	365	2	I61857
29	42	42.9	365	2	I38442

30	42	42.9	537	2	T04745
31	42	42.9	803	2	AD1282
32	42	42.9	803	2	AH1653
33	42	42.9	804	2	B89961
34	42	42.9	804	2	D69650
35	41.5	42.3	790	2	T50337
36	41	41.8	131	2	AG2115
37	41	41.8	265	2	C42595
38	41	41.8	279	2	E64109
39	41	41.8	359	2	T20575
40	41	41.8	364	2	AF2599
41	41	41.8	364	2	G97381
42	41	41.8	384	2	T08940
43	41	41.8	406	2	F96571
44	41	41.8	503	2	D96776
45	41	41.8	519	1	T02263

hypothetical prote
leucyl-tRNA synthe
leucyl-tRNA synthe
leucyl-tRNA synthe
leucine-tRNA ligas
homolog to drosoph
hypothetical prote
rfap protein - Esc
dimethylsulfoxide
hypothetical prote
probable permease
hypothetical prote
hypothetical prote
hypothetical prote
cytochrome P450 DW

ALIGNMENTS

RESULT 1

S76462
hypothetical protein - Synchocystis sp. (strain PCC 6803)

C;Species: Synchocystis sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C;Accession: S76462

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis sp.

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S76462

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-627 <KAN>

A;Cross-references: UNIPROT:P74489; UNIPARC:UPI00000C103F; EMBL:D90915; GB:AB001339; NID: A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 49.0%; Score 48; DB 2; Length 627;
Best Local Similarity 38.9%; Pred. No. 8.1;
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18

Db 597 GLEQLLGIWQLRQKFG 614

RESULT 2

A75578
transcription regulator, MarR family - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: A75578

R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; P, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A;Reference number: A75250; MUID:20036896; PMID:10567266

A;Accession: A75578

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-178 <WHI>

A;Cross-references: UNIPROT:Q9YR0; UNIPARC:UPI00000D3BE4; GB:AE001863; NID: A;Experimental source: strain R1

C;Genetics:

A;Gene: DRA0248

A;Map position: 2

Query Match 45.9%; Score 45; DB 2; Length 178;

Best Local Similarity 69.2%; Pred. No. 7.2;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 IRRFLGSIWRFIR 14
| | | | | | | |
Db 23 ILRFLGGIWRLLNR 35

RESULT 3
G64537
2-oxoglutarate/malate translocator - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: G64537
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalaf, H.G.; Glodek, A.; McKenne-son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: G64537
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-461 <TOM>
A;Cross-references: UNIPARC:UPI0000174217; GB:AE000511; TIGR:HP0143
C;Superfamily: 2-oxoglutarate/malate translocator

Query Match 44.9%; Score 44; DB 1; Length 461;
Best Local Similarity 53.8%; Pred. No. 26;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IRRFLGSIWRFIR 14
: | | | | | | | |
Db 297 VRLLSWFWRFR 309

RESULT 4
A34341
poly(3-hydroxybutyrate) synthase (EC 2.3.1.-) - Alcaligenes eutrophus
C;Species: Alcaligenes eutrophus
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C;Accession: A34341; A39190
R;Pocoles, O.P.; Sinskey, A.J.
J. Biol. Chem. 264, 15298-15303, 1989
A;Title: Poly-beta-hydroxybutyrate (PHB) biosynthesis in Alcaligenes eutrophus H16.
A;Reference number: A34341; MUID:89359357; PMID:2670936
A;Accession: A34341
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-589 <PEO>
A;Cross-references: UNIPROT:P23608; UNIPARC:UPI0000044953; GB:J05003; NID:G141958; PIDN:R;Schubert, P.; Krueger, N.; Steinbuechel, A.
J. Bacteriol. 173, 168-175, 1991
A;Title: Molecular analysis of the Alcaligenes eutrophus poly(3-hydroxybutyrate) biosynt
omoter.
A;Reference number: A39190; MUID:91100279; PMID:1987116
A;Accession: A39190
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-219 <SCH>
A;Cross-references: UNIPARC:UPI0000165162; GB:M64341; NID:G141964; PIDN:AAA21979.1; PID:
A;Note: the authors translated the codon TAC for residue 120 as Thr
C;Superfamily: poly(3-hydroxyalkanoic acid) synthase phbC
C;Keywords: acyltransferase

Query Match 44.9%; Score 44; DB 2; Length 589;
Best Local Similarity 47.6%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

QY 3 RRFLLGSIW-----RFRIFAY 17
| | | | | | | |

Db 100 RRFAGDAWRTNLPRFAAFY 120

RESULT 5
A84060
leucyl-tRNA synthetase leus [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: A84060
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A84060
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-806 <STO>
A;Cross-references: UNIPROT:Q9K758; UNIPARC:UPI0000136555; GB:AP001518; GB:BA000004; NID:
A;Experimental source: strain C-125
C;Genetics:
A;Gene: leus
C;Superfamily: leucine-tRNA ligase

Query Match 44.9%; Score 44; DB 2; Length 806;
Best Local Similarity 53.8%; Pred. No. 45;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFI 13
| | | | | | | |
Db 622 GARRFLDRVWRL 634

RESULT 6
H64102
leucine-tRNA ligase (EC 6.1.1.4) - Haemophilus influenzae (strain Rd KW20)
N;Alternate names: leucyl-tRNA synthetase
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: H64102
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuchs, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C.
A;Title: Whole genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: H64102
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-861 <TIGR>
A;Cross-references: UNIPROT:P43827; UNIPARC:UPI000013655F; GB:U32774; GB:L42023; NID:G15;
C;Genetics:
A;Gene: leus
C;Superfamily: leucine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 44.9%; Score 44; DB 2; Length 861;
Best Local Similarity 46.2%; Pred. No. 48;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFI 13
| | | | | | | |
Db 665 GAKRFLGRVWNLV 677

RESULT 7
AH3568
acriflavin resistance protein F (imported) - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AH3568
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, I.
; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesc

A;Map position: 2
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology

Query Match 43.9%; Score 43; DB 2; Length 489;
Best Local Similarity 54.5%; Pred. No. 40;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 LGSIWPIRAF 16
: : : : | : : :
Db 54 IGNNWSFLRAF 64

RESULT 10
T33269
hypothetical protein C24B9.l3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33269
R;Murray, J.; Wohldmann, P.; Langston, Y.; O'Neal, D.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid C24B9.
A;Reference number: Z21310
A;Accession: T33269
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-516 <MUR>
A;Cross-references: UNIPROT:O76442; UNIPARC:UPI000007D477; EMBL:AF068709; PID:N
A;Experimental source: strain Bristol N2; clone C24B9
C;Genetics:
A;Gene: CESP:C24B9.l3
A;Map position: 5
A;Introns: 13/3; 67/2; 116/2; 268/2; 315/2; 364/2

Query Match 43.9%; Score 43; DB 2; Length 516;
Best Local Similarity 41.2%; Pred. No. 42;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 IRRFLGSIWPIRAFYG 18
: : : : | : : :
Db 252 LKFFITSLWMFMHAFDG 268

RESULT 11
A46417
N1P1 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: nuclear import protein; protein YM9952.01c; protein YM9952.1
C;Species: Saccharomyces cerevisiae
C;Date: 21-Sep-1993 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A46417; S53979; S59302
R;Gu, Z.; Moerschell, R.P.; Sherman, F.; Goldfarb, D.S.
Proc. Natl. Acad. Sci. U.S.A. 89, 10355-10359, 1992
A;Title: N1P1, a gene required for nuclear transport in yeast.
A;Reference number: A46417; MUID:93066237; PMID:1332047
A;Accession: A46417
A;Molecule type: DNA
A;Residues: 1-812 <GUL>
A;Cross-references: UNIPROT:P32497; UNIPARC:UPI000017B2E1; EMBL:L02899
A;Note: sequence extracted from NCBI backbone (NCBI:117849, NCBIP:117850)
R;Connor, R.; Churcher, C.M.
submitted to the EMBL Data Library, April 1995
A;Reference number: S53969
A;Accession: S53979
A;Molecule type: DNA
A;Residues: 571-582,'Q','584-640,'K','642,'K','644-812 <CON>
A;Cross-references: UNIPARC:UPI0000168ACD; EMBL:Z49212; NID:g798940; PID:g79899
R;Churcher, C.M.
submitted to the EMBL Data Library, September 1995
A;Reference number: S59302
A;Accession: S59302
A;Molecule type: DNA
A;Residues: 1-110,'V','112-582,'Q','584-602 <CHU>
A;Cross-references: UNIPARC:UPI0000168ACA; EMBL:Z54141; NID:gi072408; PID:g9844
A;Experimental source: strain AB972

```
C;Genetics:
A;Gene: SGD:N1P1
A;Cross-references: SGD:S0004926; MIPS:YMR309c
A;Map position: 13R

Query Match          43.9%; Score 43; DB 2; Length 812;
Best Local Similarity 53.8%; Pred. No. 66;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 GIRFLGSIWRFI 13
    :|||::|:
Db 361 GVXKILGSIKFSV 373

RESULT 12
T04583
TMV resistance protein N homolog F23E13.30 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04583; T05507
R;Bavan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Jesse, T.
submitted to the Protein Sequence Database, March 1998
A;Reference number: 215378
A;Accession: T04583
A;Molecule type: DNA
A;Residues: 1-1607 <BEV>
A;Cross-references: UNIPROT:O65506; UNIPARC:UPI000000AA45C; EMBL:AL022141
A;Experimental source: cultivar Columbia; BAC clone F23E13
R;Bavan, M.; Wedler, H.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schueller
submitted to the Protein Sequence Database, April 1998
A;Reference number: 215418
A;Accession: T05507
A;Molecule type: DNA
A;Residues: 1448-1607 <BE2>
A;Cross-references: UNIPARC:UPI000016DBFD; EMBL:AL022373
A;Experimental source: cultivar Columbia; BAC clone T19K4
C;Genetics:
A;Map position: 4
A;Introns: 193/2; 238/2; 556/2; 930/3; 1029/3; 1287/3
A;Note: F23E13.30; T19K4.270

Query Match          43.9%; Score 43; DB 2; Length 1607;
Best Local Similarity 72.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 LGSIWRFIRAF 16
    |||||
Db 1321 LGSSWRLIRGF 1331

RESULT 13
T12085
reverse transcriptase homolog - fava bean (fragment)
C;Species: Vicia faba (fava bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12085
R;Kinoshita, T.; Wada, H.; Masaaki, I.; Shimazaki, K.
submitted to the EMBL Data Library, September 1997
A;Description: Retrotransposon-like cDNAs from guard cell protoplasts in Vicia faba.
A;Reference number: 217406
A;Accession: T12085
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-407 <KIN>
A;Cross-references: UNIPROT:O22103; UNIPARC:UPI00000A0AD3D; EMBL:AB007466; NID:d1170509;
A;Experimental source: guard cell protoplasts
C;Superfamily: pol polyprotein

Query Match          43.4%; Score 42.5; DB 2; Length 407;
Best Local Similarity 57.9%; Pred. No. 40;
Matches 11; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

QY 1 GIRFLGSIW---RFIRAF 16
    |||||

C;Genetics:
A;Gene: SGD:N1P1
A;Cross-references: SGD:S0004926; MIPS:YMR309c
A;Map position: 13R

Query Match          43.9%; Score 43; DB 2; Length 812;
Best Local Similarity 53.8%; Pred. No. 66;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 GIRFLGSIWRFI 13
    :|||::|:
Db 361 GVXKILGSIKFSV 373

RESULT 14
E84953
penicillin-binding protein 1b [imported] - Buchnera sp. (strain APS)
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C;Accession: E84953
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A1
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: E84953
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-760 <STO>
A;Cross-references: UNIPARC:UPI000005E4C8; GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: mrcB; BU200
C;Superfamily: penicillin-binding protein 1B

Query Match          43.4%; Score 42.5; DB 2; Length 760;
Best Local Similarity 44.4%; Pred. No. 74;
Matches 8; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 2 IRRFL-GSIWRFIRAFYG 18
    ||||:|:|:|:|
Db 32 INRFINGKWNPFPSIYG 49

RESULT 15
T52113
probable transcription co-activator KIWI [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Accession: T52113
R;Cormack, R.S.; Hahlbrock, K.; Somesich, I.E.
Plant J. 14, 685-92, 1998
A;Title: Isolation of putative plant transcriptional coactivators using a modified two-hy
A;Reference number: Z25848; MUID:98346011; PMID:9681033
A;Accession: T52113
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-107 <COR>
A;Cross-references: UNIPROT:O65154; UNIPARC:UPI000000C45F; EMBL:AF053302; PIDN:AAC08574.J
A;Experimental source: cultivar Columbia
C;Genetics:
A;Gene: KIWI
A;Map position: V
C;Function:
A;Description: probably plays a role in gene activation during pathogen defence and plant
C;Superfamily: Caenorhabditis elegans hypothetical protein T13F2.2

Query Match          42.9%; Score 42; DB 2; Length 107;
Best Local Similarity 50.0%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 IRRFLGSIWRFIRAFY 17
    :||:|:|:|:|
Db 54 VRNNGKIIDIREFY 69

Search completed: May 19, 2006, 14:39:59
Job time : 15.2857 secs
```

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:13:32 ; Search time 115.429 Seconds
(without alignments)
144.247 Million cell updates/sec

Title: US-10-712-447-10
Perfect score: 98
Sequence: 1 GIRFLGSIWRFAYG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92501592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	59.2	805	2	Q3APV5_CHLCH
2	54	55.1	670	2	Q25271_LEPDE
3	52	53.1	735	2	Q9F7V7_RHLIV
4	52	53.1	805	2	Q44QD1_CHLLI
5	52	53.1	816	2	Q43K01_9CHLB
6	51	52.0	407	2	Q39L57_BURS3
7	51	52.0	408	2	Q456F4_9BURK
8	51	52.0	408	2	Q4LK44_9BURK
9	50	51.0	579	1	Q3R7_HUMAN
10	50	51.0	579	1	Q3R7_PANTR
11	50	51.0	580	1	Q3R7_MOUSE
12	50	51.0	580	1	Q3R7_RAT
13	49	50.0	409	2	Q4BFM2_BURVI
14	49	50.0	449	2	Q3PK79_PARDE
15	49	50.0	488	2	Q84ZM1_PEA
16	48	49.0	188	2	Q3ILN7_9DELT
17	48	49.0	298	2	Q8R587_MOUSE
18	48	49.0	435	2	Q2JIT0_9CYAN
19	48	49.0	578	1	Q3R6_TETNG
20	48	49.0	578	2	Q5GH49_FUGRU
21	48	49.0	627	2	P74489_SVNY3
22	47.5	48.5	240	2	P97035_HAESO
23	47.5	48.5	577	2	Q36XB4_RHOPA
24	47.5	48.5	577	2	Q37C12_RHOPD
25	47.5	48.5	807	2	Q3VMG0_9CHLB
26	47	48.0	486	2	Q5U4I4_XENLA
27	47	48.0	487	2	Q32N49_XENLA
28	47	48.0	910	2	Q5ZDS6_ORYSA
29	46	46.9	361	2	Q2NUB5_SODGL
30	46	46.9	385	2	Q5ZPA2_9DELT
31	46	46.9	540	2	Q5GH65_MOUSE

32 46 46.9 580 2 Q5GH40_BRARE
33 46 46.9 638 1 XKR6_RAT
34 46 46.9 641 1 XKR6_HUMAN
35 46 46.9 807 1 SYL_CHLTE
36 46 46.9 836 2 Q2Y8V4_NITMU
37 46 46.9 859 2 Q3XW00_9PROT
38 46 46.9 863 2 Q2S415_9SPHI
39 46 46.9 2484 2 Q5CP27_CRYPV
40 45 45.9 178 2 Q9RYR0_DEIRA
41 45 45.9 219 2 Q6LIT5_PICVO
42 45 45.9 276 2 Q4BS81_BURVI
43 45 45.9 278 2 Q7VW93_BORPE
44 45 45.9 278 2 Q7W7P3_BORPE
45 45 45.9 278 2 Q7WL31_BORBR

ALIGNMENTS

RESULT 1
Q3APV5_CHLCH
ID Q3APV5_CHLCH PRELIMINARY; PRT; 805 AA.
AC Q3APV5_2005, integrated into UniProtKB/TrEMBL.
DT 22-NOV-2005, sequence version 1.
DT 21-FEB-2006, entry version 5.
DE Leucyl-tRNA synthetase class Ia (EC 6.1.1.4).
GN OrderedLocusNames=Cag_1688;
OS Chlorobium chlorochromatii (strain Cad3).
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium/Pelodictyon group; Chlorobium.
OX NCBI_TaxID=340177;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG US DOE Joint Genome Institute; Barry K., Dettler J.C., Glavina T.,
RA Copeland A., Lucas S., Lapidus S., Bryant D., Schmutz J., Larimer F.,
RA Hammon N., Israni S., Pitluck S., Ivanova N., Richardson P.,
RA Land M., Kyripides N., Ivanova N., Richardson P.,
RT "Complete sequence of Chlorobium chlorochromatii Cad3.";
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL: CP000108; ABB28940.1; -; Genomic_DNA.
DR GO: GO:0005524; F-ATP binding; IEA.
DR GO: GO:0004823; F:leucine-tRNA ligase activity; IEA.
DR GO: GO:0016874; F:ligase activity; IEA.
DR GO: GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
KW Aminoacyl-tRNA synthetase; Complete proteome; Ligase.
SQ SEQUENCE 805 AA; 92007 MW; AOC78B83732AF54C CRC64;

Query Match 59.2%; Score 58; DB 2; Length 805;
Best Local Similarity 63.2%; Pred. No. 3.2;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GIRFLGSIWRFI 13
||| ||| ||| ||| |||
Db 622 GISRFLGKWRFFV 634

RESULT 2
Q25271_LEPDE
ID Q25271_LEPDE PRELIMINARY; PRT; 670 AA.
AC Q25271_1
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Diapause protein 1 (Fragment).
GN Name=Dp19;
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;

OC Chrysomeloidea; Chrysomelidae; Chrysomelinae; Doryphorini;
 OC Leptinotarsa.
 OX NCBI_TaxID=7539;
 RN [1]
 RA NUCLEOTIDE SEQUENCE.
 de Kort C.A.D., Koopmanschap A.B.;
 RT "Nucleotide and deduced amino acid sequence of a cDNA clone encoding
 RT diapause protein 1, an amylphorin-type storage hexamer of the Colorado
 RT potato beetle.";
 RL J. Insect Physiol. 40:527-535(1994).
 CC -----
 CC Copyrighted by the Uniprot Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; X76080; CAA53691.1; -; mRNA.
 DR HSP; P04253; ILL1.
 DR GO; GO:0005344; F:oxygen transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR GO; GO:000896; Hemocyanin.
 DR InterPro; IPR000896; Hemocyanin_C.
 DR InterPro; IPR005203; hemocyanin_N.
 DR PANTHER; PTHR11511; Hemocyanin; 1.
 DR Pfam; PF03723; Hemocyanin_C; 1.
 DR Pfam; PF03722; Hemocyanin_M; 1.
 DR Pfam; PF03722; Hemocyanin_N; 1.
 DR PRINTS; PR00187; HAEMOCYANIN.
 DR PROSITE; PS00210; HEMOCYANIN_2; UNKNOWN_1.
 FT NON TER 1
 SQ SEQUENCE 670 AA; 79825 MW; 8A000BAll15BEC8A6 CRC64;

Query Match 55.1%; Score 54; DB 2; Length 670;
 Best Local Similarity 43.8%; Pred. No. 11;
 Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 3 RRFGLSIWRFIRAFY 18
 | | | | | : | | | | | : | |
 351 RKFGALMSYLRHFFG 366

Db

RESULT 3
 Q9F7V7 RHILV PRELIMINARY; PRT; 735 AA.
 AC Q9F7V7;
 DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
 DT 01-MAR-2001, sequence version 1.
 DT 07-FEB-2006, entry version 25.
 DE ABC transporter RzcB.
 GN Name=rzcB;
 OS Rhizobium leguminosarum bv. viciae.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=387;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=305;
 RX MEDLINE=21360352; PubMed=11467725; DOI=10.1139/cjm-47-6-495;
 RA Venter A.P., Twelker S., Orenik I.J., Hynes M.F.;
 RT "Analysis of the genetic region encoding a novel rhizobiocin from
 RT Rhizobium leguminosarum bv. viciae strain 305.";
 RL Can. J. Microbiol. 47:495-502(2001).
 CC -----
 CC Copyrighted by the Uniprot Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AF273216; AAG25076.1; -; Genomic_DNA.
 DR HSP; P08716; 1MT0.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0016887; F:ATPase activity; IEA.
 DR GO; GO:0042262; F:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO; GO:0000466; F:nucleotide binding; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0008565; F:protein transporter activity; IEA.

DR GO; GO:0015031; P:protein transport; IEA.
 DR GO; GO:0008508; P:proteolysis; IEA.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR011527; ABC_TM_1.
 DR InterPro; IPR001140; ABC_TM_transpt.
 DR InterPro; IPR003439; ABC_transp_like.
 DR InterPro; IPR005074; Peptidase_C39.
 DR InterPro; PTHR101132; Type_I_sec_HlyB.
 DR PANTHER; PTHR19242:SF74; Type_I_sec_HlyB; 1.
 DR Pfam; PF00664; ABC_membrane; 1.
 DR Pfam; PF00005; ABC_tran; 1.
 DR Pfam; PF03412; Peptidase_C39; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR TIGRFAMS; TIGR01846; type_I_sec_HlyB; 1.
 DR PROSITE; PS50929; ABC_TMIF; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
 DR PROSITE; PS50990; PEPTIDASE_C39; 1.
 DR PROSITE; PS50990; PEPTIDASE_C39; 1.
 SQ SEQUENCE 735 AA; 80717 MW; 0216259241F3630C CRC64;

Query Match 53.1%; Score 52; DB 2; Length 735;
 Best Local Similarity 52.5%; Pred. No. 26;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAF 16
 | | | | | : | | | | | : | |
 161 GRRFLPFAIWRRAAF 176

Db

RESULT 4
 Q44QD1 CHLLI PRELIMINARY; PRT; 805 AA.
 AC Q44QD1;
 DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
 DT 13-SEP-2005, sequence version 1.
 DT 21-FEB-2006, entry version 9.
 DE Leucyl-tRNA synthetase bacterial/mitochondrial, class Ia.
 DE ORFNames=ClmdRAFT_1980;
 OS Chlorobium limicola DSM 245.
 OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
 OC Chlorobium/Pelodictyon group; Chlorobium.
 OX NCBI_TaxID=290315;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=DSM 245;
 RG US DOE Joint Genome Institute (JGI-PGF);
 RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
 RA Hammon N., Israni S., Pitluck S., Richardson P.;
 RT "Sequencing of the draft genome and assembly of Chlorobium limicola
 RT DSM 245.";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=DSM 245;
 RG US DOE Joint Genome Institute (JGI-ORNL);
 RA Larimer P., Land W.;
 RT "Annotation of the draft genome assembly of Chlorobium limicola DSM
 RT 245.";
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -----
 CC Copyrighted by the Uniprot Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AAJ0100009; EAM43320.1; -; Genomic_DNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
 DR GO; GO:0006429; F:leucyl-tRNA aminoacylation; IEA.
 DR InterPro; IPR02302; Leu_tRNAasyt_1a.
 DR Pfam; PF00133; tRNA-synt_1; 1.

```
DR PRINTS; PR00985; TRNASYNTHLEU.
KW Aminoacyl-tRNA synthetase_bact; 1.
SQ SEQUENCE 805 AA; 91997 MW; D4P3FE28F9E92DF3 CRC64;

Query Match 53.1%; Score 52; DB 2; Length 805;
Best Local Similarity 61.5%; Pred. No. 29;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFI 13
|||:||||:|:|:|
Db 622 GISRPLGKVMRLV 634

RESULT 5
Q43K01_9CHLB PRELIMINARY; PRT; 816 AA.
ID Q43K01_9CHLB
AC Q43K01
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, entry version 9.
DE Leucyl-tRNA synthetase bacterial/mitochondrial, class Ia.
GN ORFNames=Cpha266DRAFT_2546;
OS Chlorobium phaeobacteroides DSM 266.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium/Pelodictyon group; Chlorobium.
OX NCBI_TaxID=290317;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 266;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hamon N., Israni S., Pitluck S., Richardson P.,
RT "Sequencing of the draft genome and assembly of Chlorobium
RT phaeobacteroides DSM 266.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 266;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Chlorobium
RT phaeobacteroides DSM 266.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; AAIB01000002; EAMJ5935.1; -; Genomic_DNA.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
DR GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
DR InterPro; IPR002302; Leu_tRNAsyn_1a.
DR Pfam; PF00133; tRNA-synt_1; 1.
DR PRINTS; PR00985; TRNASYNTHLEU.
DR TIGRFAMs; TIGR00396; leus_bact; 1.
KW Aminoacyl-tRNA synthetase.
SQ SEQUENCE 816 AA; 93335 MW; 6770B1DAC50560F1 CRC64;

Query Match 53.1%; Score 52; DB 2; Length 816;
Best Local Similarity 61.5%; Pred. No. 29;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFI 13
|||:||||:|:|:|
Db 622 GISRPLGKVMRLV 634

RESULT 6
Q39L57_BURS3 PRELIMINARY; PRT; 407 AA.
ID Q39L57
AC Q39L57
DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, entry version 4.
DE Hypothetical protein.
GN OrderedLocusNames=cepl8194_A3207;
OS Burkholderia sp. (strain 383) (Burkholderia cepacia (strain ATCC 17760
/ NCIB 9086 / R18194)).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=269483;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hamon N., Israni S., Pitluck S., Chain P., Malfatti S., Shin M.,
RA Vergez L., Schmutz J., Larimer F., Land M., Kyrpides N., Lykidis A.,
RA Richardson P.;
RT "Complete sequence of chromosome 1 of Burkholderia sp. 383.";
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; CP000151; AB806809.1; -; Genomic_DNA.
DR Complete proteome; Hypothetical protein.
KW SEQUENCE 407 AA; 45483 MW; 957829B27BCABFC1 CRC64;

Query Match 52.0%; Score 51; DB 2; Length 407;
Best Local Similarity 47.1%; Pred. No. 20;
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFY 17
|||:||||:|:|:|
Db 327 GIROMLGHVWOWTRSSY 343

RESULT 7
Q456F4_9BURK PRELIMINARY; PRT; 408 AA.
ID Q456F4_9BURK
AC Q456F4
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Hypothetical protein.
GN ORFNames=BcendRAFT_3751;
OS Burkholderia cenocepacia AU 1054.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=331271;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AU 1054;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hamon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT AU 1054.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AU 1054;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT AU 1054.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
```

```

CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AAH101000010; EMBL2352.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 408 AA; 45545 MW; 3C2BCA9471BAAE93 CRC64;
Query Match 52.0%; Score 51; DB 2; Length 408;
Best Local Similarity 47.1%; Pred. No. 20;
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GIRREFLGSWIRAFY 17
|||:|:|:|:|:|
Db 328 GIRQMLGHVQWTRSS 344

RESULT 8
Q4LK44_9BURK PRELIMINARY; PRT; 408 AA.
AC Q4LK44;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Hypothetical protein.
OS ORFNames=Bcen2424DRAFT 1071;
GN Burkholderia cenocepacia HI2424.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OC NCBI_TaxID=331272;
[1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=HI2424;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT HI2424."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HI2424;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT HI2424."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AAHL01000063; EMBL16412.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 408 AA; 45603 MW; 7F393888305911D2 CRC64;
Query Match 52.0%; Score 51; DB 2; Length 408;
Best Local Similarity 47.1%; Pred. No. 20;
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GIRREFLGSWIRAFY 17
|||:|:|:|:|:|
Db 328 GIRQMLGHVQWTRSS 344

RESULT 9
XK77_HUMAN
ID -XK77_HUMAN STANDARD; PRT; 579 AA.
AC Q5GH72; Q9NUG5;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE XK-related protein 7.

```

```

GN Name=XK77; Synonyms=C20orf159, XK77;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE [MRNA].
RP Huang C.-H., Chen Y.;
RT "A superfamily of XK-related genes (XRG) widely expressed in
RT vertebrates and invertebrates."
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Levaeslaih M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.I., McConnachie L.J., McMay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Suce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20."
RL Nature 414:865-871(2001).
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -!- SIMILARITY: Belongs to the XK family.
CC -!- CAUTION: Ref.2 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY534245; AAT07094.1; -; mRNA.
DR EMBL; AL031658; CAB88102.1; ALT_SEQ; Genomic_DNA.
DR Ensembl; ENSG00000101321; Homo sapiens.
DR HGNC; HGNC:23062; XK77.
KW Membrane; Transmembrane.
FT CHAIN 1 579 XK-related protein 7.
FT /FTID=PRO_0000190788.
FT TRANSMEM 59 79 Potential.
FT TRANSMEM 89 109 Potential.
FT TRANSMEM 260 280 Potential.
FT TRANSMEM 314 334 Potential.
FT TRANSMEM 355 375 Potential.
FT TRANSMEM 384 404 Potential.
FT TRANSMEM 415 435 Potential.
SQ SEQUENCE 579 AA; 63826 MW; D8D0FF64B9EDD53D CRC64;
Query Match 51.0%; Score 50; DB 1; Length 579;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 LGSWIRAFY 17
|||:|:|:|:|

```

```
Db      190 LGQVWRYLRALY 201

RESULT 10
ID -XKR7 PANTR          STANDARD;          PRT;    579 AA.
AC      O49LS1;
DT      11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT      13-SEP-2005, sequence version 1.
DT      07-FEB-2006, entry version 6.
DE      XK-related protein 7.
GN      Name=XKR7; Synonyms=XRG7;
OS      Pan troglodytes (Chimpanzee).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC      Pan.
OX      NCBI_TaxID=9598;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [MRNA].
RA      Huang C.-H., Chen Y.;
RT      "A superfamily of XK-related genes (XRG) widely expressed in
RT      vertebrates and invertebrates.";
RL      Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC      -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC      (Potential).
CC      -!- SIMILARITY: Belongs to the XK family.
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; AY702910; AAV83783.1; -; mRNA.
KW      Membrane; Transmembrane.
FT      CHAIN          1          579
FT      TRANSMEM      59          79
FT      TRANSMEM      89          109
FT      TRANSMEM      260         280
FT      TRANSMEM      314         334
FT      TRANSMEM      355         375
FT      TRANSMEM      384         404
FT      TRANSMEM      415         435
SQ      SEQUENCE 579 AA; 63593 MW; 6DFE1191093B5D4 CRC64;

Query Match          51.0%; Score 50; DB 1; Length 579;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      6 LGSWRFIRAFY 17
      |||:|:|:|
Db      190 LGQVWRYLRALY 201

RESULT 12
XKR7_RAT
ID -XKR7 RAT          STANDARD;          PRT;    580 AA.
AC      Q5GH56;
DT      11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT      01-MAR-2005, sequence version 1.
DT      07-FEB-2006, entry version 8.
DE      XK-related protein 7.
GN      Name=Xkr7; Synonyms=Xrg7;
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridea; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [MRNA].
RA      Huang C.-H., Chen Y.;
RT      "A superfamily of XK-related genes (XRG) widely expressed in
RT      vertebrates and invertebrates.";
RL      Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC      -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC      (Potential).
CC      -!- SIMILARITY: Belongs to the XK family.
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; AY534261; AAT07110.1; -; mRNA.
KW      Membrane; Transmembrane.
FT      CHAIN          1          580
FT      TRANSMEM      59          79
FT      TRANSMEM      89          109
FT      TRANSMEM      260         280
FT      TRANSMEM      303         323
FT      TRANSMEM      326         346
FT      TRANSMEM      355         375
FT      TRANSMEM      384         404
FT      TRANSMEM      415         435
SQ      SEQUENCE 580 AA; 64302 MW; F3291FABF4C5A826 CRC64;

Query Match          51.0%; Score 50; DB 1; Length 580;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      6 LGSWRFIRAFY 17
      |||:|:|:|
Db      190 LGQVWRYLRALY 201

RESULT 11
XKR7_MOUSE
ID -XKR7 MOUSE        STANDARD;          PRT;    580 AA.
AC      Q5GH54;
DT      11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT      01-MAR-2005, sequence version 1.
DT      07-FEB-2006, entry version 10.
DE      XK-related protein 7.
GN      Name=Xkr7; Synonyms=Xrg7;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridea; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [MRNA].
RA      Huang C.-H., Chen Y.;
RT      "A superfamily of XK-related genes (XRG) widely expressed in
RT      vertebrates and invertebrates.";
RL      Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC      -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC      (Potential).
CC      -!- SIMILARITY: Belongs to the XK family.
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; AY534261; AAT07110.1; -; mRNA.
KW      Membrane; Transmembrane.
FT      CHAIN          1          580
FT      TRANSMEM      59          79
FT      TRANSMEM      89          109
FT      TRANSMEM      260         280
FT      TRANSMEM      303         323
FT      TRANSMEM      326         346
FT      TRANSMEM      355         375
FT      TRANSMEM      384         404
FT      TRANSMEM      415         435
SQ      SEQUENCE 580 AA; 64338 MW; 8F4907F391B4F5BE CRC64;
```



```

DT 07-FEB-2006, entry version 4.
DE Cytochrome P450.
OS CYPNames=PdenDRAFT_4722;
GN Paracoccus denitrificans PD1222.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Paracoccus.
OC NCBI_TaxID=318586;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PD1222;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RA "Sequencing of the draft genome and assembly of Paracoccus
RT denitrificans PD1222.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PD1222;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Paracoccus denitrificans
RT PD1222.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -! SIMILARITY: Belongs to the cytochrome P450 family.
CC -----
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AAIT01000001; EAN68115.1; -; Genomic_DNA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002401; EP450I.
DR Pfam; PF00067; P450.1.
DR PRINTS; PR00463; EP450I.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
KW HEME; Iron; Metal-binding; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 449 AA; 50659 MW; 5F3EEC9E12AA3B35 CRC64;

Query Match 50.0%; Score 49; DB 2; Length 449;
Best Local Similarity 64.3%; Pred.No. 46;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 RRFGLSGIWRIFRAF 16
| : ||:|||||
Db 9 RQGRGSVWRIFRDF 22

RESULT 15
ID Q84ZW1_PEA PRELIMINARY; PRT; 488 AA.
OS Q84ZW1;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Ent-kaurenoic acid oxidase.
GN Name=KAOL;
OS Pistum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OC NCBI_TaxID=3888;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Shoot;

```



```

RX MEDLINE=22417727; PubMed=12529541; DOI=10.1104/pp.012963;
RA Davidson S.E., Elliott R.C., Helliwell C.A., Poole A.T., Reid J.B.;
RT "The pea gene NA encodes ent-kaurenoic acid oxidase.";
RL Plant Physiol. 131:335-344(2003).
CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum (By
CC similarity).
CC -!- SIMILARITY: Belongs to the cytochrome P450 family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AF37321; AA023063.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR02401; EP450I.
DR PANTHER; PTHR19383; Cytochrome_P450; 1.
DR Pfam; PF00067; P450; 2.
DR PRINTS; PR00463; EP450I.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
KW Endoplasmic reticulum; Heme; Iron; Membrane; Metal-binding;
KW Monooxygenase; Oxidoreductase.
SQ SEQUENCE 488 AA; 56478 MW; 503453CB6E43C830 CRC64;

```

```

Query Match          50.0%; Score 49; DB 2; Length 488;
Best Local Similarity 58.3%; Pred. No. 50;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 5 FLGSIWRFIRAF 16
   |:|:| |:|
Db 54 FIGNWSFLRAF 65

```

Search completed: May 19, 2006, 14:38:15
Job time : 116.429 secs

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:38:42 ; Search time 24.8571 Seconds
(without alignments)

63.384 Million cell updates/sec

Title: US-10-712-447-10

Perfect score: 98

Sequence: 1 GRRFLGSIWRFIRAPYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5 COMB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS COMB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE COMB.pep.*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	79.6	18	2	US-08-940-095-242
2	78	79.6	18	2	US-08-940-093-242
3	78	79.6	18	2	US-08-940-096-242
4	78	79.6	18	2	US-09-465-719-242
5	78	79.6	18	2	US-09-453-605-242
6	78	79.6	18	2	US-09-453-838-242
7	78	79.6	18	2	US-08-940-136-242
8	78	79.6	18	2	US-09-453-841-242
9	78	79.6	18	2	US-09-453-833-242
10	78	79.6	18	2	US-09-453-826-242
11	78	79.6	18	2	US-09-453-840-242
12	78	79.6	18	2	US-09-865-989-242
13	78	79.6	18	2	US-09-453-834-242
14	78	79.6	18	2	US-10-283-599-242
15	78	79.6	18	2	US-09-465-718-242
16	51	52.0	76	2	US-09-205-258-892
17	51	52.0	76	2	US-10-004-860-892
18	47.5	48.5	253	2	US-09-586-106D-49
19	47.5	48.5	253	2	US-10-799-870-49
20	45.5	46.4	254	2	US-09-586-106D-45
21	45.5	46.4	254	2	US-10-799-870-45
22	45	45.9	22	1	US-08-338-882-40
23	45	45.9	22	1	US-08-338-882-41
24	45	45.9	539	2	US-09-710-279-340
25	45	45.9	835	2	US-09-134-001C-5105
26	45	45.9	877	2	US-09-328-352-8162

27 44 44.9 22 1 US-08-132-767-50 Sequence 50, Appl
28 44 44.9 589 1 US-08-756-317-5 Sequence 5, Appl
29 44 44.9 1052 2 US-09-134-000C-6620 Sequence 6620, Ap
30 43 43.9 23 3 US-10-160-101-83 Sequence 83, Appl
31 43 43.9 413 3 US-09-609-146-27 Sequence 27, Appl
32 43 43.9 439 3 US-09-609-146-29 Sequence 29, Appl
33 43 43.9 683 2 US-09-902-540-15932 Sequence 15932, A
34 43 43.9 702 2 US-10-094-749-2262 Sequence 2262, Ap
35 43 43.9 812 2 US-09-538-092-643 Sequence 643, Ap
36 42 42.9 14 1 US-08-480-190-3 Sequence 3, Appl
37 42 42.9 14 1 US-08-488-379-3 Sequence 3, Appl
38 42 42.9 14 2 US-08-475-399A-3 Sequence 3, Appl
39 42 42.9 14 2 US-08-077-255A-3 Sequence 3, Appl
40 42 42.9 14 5 PCT-US93-07545-3 Sequence 3, Appl
41 42 42.9 15 1 US-08-480-190-2 Sequence 2, Appl
42 42 42.9 15 1 US-08-488-379-2 Sequence 2, Appl
43 42 42.9 15 2 US-08-475-399A-2 Sequence 2, Appl
44 42 42.9 15 2 US-08-077-255A-2 Sequence 2, Appl
45 42 42.9 15 5 PCT-US93-07545-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-940-095-242
; Sequence 242, Application US/08940095
; Patent No. 6004925
; GENERAL INFORMATION:
; APPLICANT: Daseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttnet, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,095
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6004925e
US-08-940-095-242

Query Match 79.6%; Score 78; DB 2; Length 18;
 Best Local Similarity 72.2%; Pred. No. 1.1e-05;
 Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 G1RRFLGSIWRFIRAFVG 18
 ||:|||||:|:|
 Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 2
 US-08-940-093-242
 ; Sequence 242, Application US/08940093
 ; Patent No. 6037323
 ; GENERAL INFORMATION:
 ; APPLICANT: Dasseux, Jean-Louis
 ; APPLICANT: Sekul, Renate
 ; APPLICANT: Buttner, Klaus
 ; APPLICANT: Cornut, Isabelle
 ; APPLICANT: Metz, Gunther
 ; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
 ; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
 ; NUMBER OF SEQUENCES: 258
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036-2811
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/940,093
 ; FILING DATE: 29-SEP-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 009196-0006-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-493-4935
 ; TELEFAX: 650-493-5556
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 242:
 ; LENGTH: 18 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: NO. 6037323e
 ; US-08-940-093-242

Query Match 79.6%; Score 78; DB 2; Length 18;
 Best Local Similarity 72.2%; Pred. No. 1.1e-05;
 Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 G1RRFLGSIWRFIRAFVG 18
 ||:|||||:|:|
 Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 3
 US-08-940-096-242
 ; Sequence 242, Application US/08940096
 ; Patent No. 6046166
 ; GENERAL INFORMATION:
 ; APPLICANT: Dasseux, Jean-Louis
 ; APPLICANT: Sekul, Renate
 ; APPLICANT: Buttner, Klaus
 ; APPLICANT: Cornut, Isabelle
 ; APPLICANT: Metz, Gunther
 ; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
 ; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
 ; NUMBER OF SEQUENCES: 258
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036-2811

Query Match 79.6%; Score 78; DB 2; Length 18;
 Best Local Similarity 72.2%; Pred. No. 1.1e-05;
 Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 G1RRFLGSIWRFIRAFVG 18
 ||:|||||:|:|
 Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 4
 US-09-465-719-242
 ; Sequence 242, Application US/09465719
 ; Patent No. 6265377
 ; GENERAL INFORMATION:
 ; APPLICANT: Dasseux, Jean-Louis
 ; APPLICANT: Sekul, Renate
 ; APPLICANT: Buttner, Klaus
 ; APPLICANT: Cornut, Isabelle
 ; APPLICANT: Metz, Gunther
 ; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
 ; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
 ; NUMBER OF SEQUENCES: 258
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036-2811

Query Match 79.6%; Score 78; DB 2; Length 18;
 Best Local Similarity 72.2%; Pred. No. 1.1e-05;
 Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 G1RRFLGSIWRFIRAFVG 18
 ||:|||||:|:|
 Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 5
 US-08-940-096-242
 ; Sequence 242, Application US/08940096
 ; Patent No. 6046166
 ; GENERAL INFORMATION:
 ; APPLICANT: Dasseux, Jean-Louis
 ; APPLICANT: Sekul, Renate
 ; APPLICANT: Buttner, Klaus
 ; APPLICANT: Cornut, Isabelle
 ; APPLICANT: Metz, Gunther
 ; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
 ; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
 ; NUMBER OF SEQUENCES: 258
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036-2811

APPLICANT: Dasseux, Jean-Louis
 APPLICANT: Sekul, Renate
 APPLICANT: Buttner, Klaus
 APPLICANT: Cornut, Isabelle
 APPLICANT: Metz, Gunther
 TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
 TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
 NUMBER OF SEQUENCES: 258
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds LLP
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036-2811
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/940,096
 FILING DATE: 29-SEP-1997
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 009196-0005-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-493-4935
 TELEFAX: 650-493-5556
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 242:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: NO. 6046166e
 US-08-940-096-242

Query Match 79.6%; Score 78; DB 2; Length 18;
 Best Local Similarity 72.2%; Pred. No. 1.1e-05;
 Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 G1RRFLGSIWRFIRAFVG 18
 ||:|||||:|:|
 Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 6
 US-09-465-719-242
 ; Sequence 242, Application US/09465719
 ; Patent No. 6265377
 ; GENERAL INFORMATION:
 ; APPLICANT: Dasseux, Jean-Louis
 ; APPLICANT: Sekul, Renate
 ; APPLICANT: Buttner, Klaus
 ; APPLICANT: Cornut, Isabelle
 ; APPLICANT: Metz, Gunther
 ; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
 ; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
 ; NUMBER OF SEQUENCES: 258
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036-2811

Query Match 79.6%; Score 78; DB 2; Length 18;
 Best Local Similarity 72.2%; Pred. No. 1.1e-05;
 Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 G1RRFLGSIWRFIRAFVG 18
 ||:|||||:|:|
 Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 7
 US-08-940-096-242
 ; Sequence 242, Application US/08940096
 ; Patent No. 6046166
 ; GENERAL INFORMATION:
 ; APPLICANT: Dasseux, Jean-Louis
 ; APPLICANT: Sekul, Renate
 ; APPLICANT: Buttner, Klaus
 ; APPLICANT: Cornut, Isabelle
 ; APPLICANT: Metz, Gunther
 ; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
 ; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
 ; NUMBER OF SEQUENCES: 258
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036-2811

Query Match 79.6%; Score 78; DB 2; Length 18;
 Best Local Similarity 72.2%; Pred. No. 1.1e-05;
 Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 G1RRFLGSIWRFIRAFVG 18
 ||:|||||:|:|
 Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 8
 US-09-465-719-242
 ; Sequence 242, Application US/09465719
 ; Patent No. 6265377
 ; GENERAL INFORMATION:
 ; APPLICANT: Dasseux, Jean-Louis
 ; APPLICANT: Sekul, Renate
 ; APPLICANT: Buttner, Klaus
 ; APPLICANT: Cornut, Isabelle
 ; APPLICANT: Metz, Gunther
 ; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
 ; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
 ; NUMBER OF SEQUENCES: 258
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036-2811

Query Match 79.6%; Score 78; DB 2; Length 18;
 Best Local Similarity 72.2%; Pred. No. 1.1e-05;
 Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 G1RRFLGSIWRFIRAFVG 18
 ||:|||||:~:~
 Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 9
 US-08-940-096-242
 ; Sequence 242, Application US/08940096
 ; Patent No. 6046166
 ; GENERAL INFORMATION:
 ; APPLICANT: Dasseux, Jean-Louis
 ; APPLICANT: Sekul, Renate
 ; APPLICANT: Buttner, Klaus
 ; APPLICANT: Cornut, Isabelle
 ; APPLICANT: Metz, Gunther
 ; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
 ; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
 ; NUMBER OF SEQUENCES: 258
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036-2811

Query Match 79.6%; Score 78; DB 2; Length 18;
 Best Local Similarity 72.2%; Pred. No. 1.1e-05;
 Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 G1RRFLGSIWRFIRAFVG 18
 ||:|||||:~:~
 Db 1 G1KKFLGSIWKFIKAFVG 18

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/465,719
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,093
FILING DATE: 29-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6265377e
US-09-465-719-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFVG 18
||:|||||:|:|
Db 1 GIKFLGSIWKFIRAFVG 18

RESULT 5
US-09-453-605-242
Sequence 242, Application US/09453605
Patent No. 6329341
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
Sekul, Renate
Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,605
FILING DATE: 26-NOV-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6329341e
SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-453-605-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFVG 18
||:|||||:|:|
Db 1 GIKFLGSIWKFIRAFVG 18

RESULT 6
US-09-453-838-242
Sequence 242, Application US/09453838
Patent No. 6376464
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
Sekul, Renate
Buttner, Klaus
Cornut, Isabelle
Metz, Gunther
Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,838
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6376464e

US-09-453-838-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFGLSIWRFTRAFVG 18
||:|||||:||||:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 7

US-08-940-136-242
; Sequence 242, Application US/08940136
; Patent No. 6518412
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,136
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0007-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6518412e
; US-08-940-136-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFGLSIWRFTRAFVG 18
||:|||||:||||:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 8

US-09-453-841-242

; Sequence 242, Application US/09453841

; Patent No. 6573239
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,841
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6573239e
; US-09-453-841-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFGLSIWRFTRAFVG 18
||:|||||:||||:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 9

US-09-453-833-242
; Sequence 242, Application US/09453833
; Patent No. 6602854
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453.833
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6602854e
US-09-453-833-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFVG 18
||:|||||:|:|
Db 1 GIKKFLGSIWKFIRAFVG 18

RESULT 10
US-09-453-826-242
Sequence 242, Application US/09453826
Patent No. 6630450
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453.826
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6630450e
US-09-453-826-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFVG 18
||:|||||:|:|
Db 1 GIKKFLGSIWKFIRAFVG 18

RESULT 11
US-09-453-840-242
Sequence 242, Application US/09453840
Patent No. 6716816
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453.840
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids

```
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6716816e
US-09-453-840-242
  Query Match          79.6%; Score 78; DB 2; Length 18;
  Best Local Similarity 72.2%; Pred. No. 1.1e-05;
  Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRREFLGSIWRFIRAFYG 18
    ||::|||||::|::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 12
US-09-865-989-242
; Sequence 242, Application US/09865989
; Patent No. 6734169
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,989
; FILING DATE: 25-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/465,719
; FILING DATE: 17-DEC-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6734169e
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-865-989-242
  Query Match          79.6%; Score 78; DB 2; Length 18;
  Best Local Similarity 72.2%; Pred. No. 1.1e-05;
  Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRREFLGSIWRFIRAFYG 18
    ||::|||||::|::|
Db 1 GIKKFLGSIWKFIKAFVG 18
```

```
RESULT 13
US-09-453-834-242
; Sequence 242, Application US/09453834
; Patent No. 6753313
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,834
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6753313e
US-09-453-834-242
  Query Match          79.6%; Score 78; DB 2; Length 18;
  Best Local Similarity 72.2%; Pred. No. 1.1e-05;
  Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRREFLGSIWRFIRAFYG 18
    ||::|||||::|::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 14
US-10-283-599-242
; Sequence 242, Application US/10283599
; Patent No. 6844327
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
```


;; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.

;; NUMBER OF SEQUENCES: 274

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Pennie & Edmonds LLP

;; STREET: 1155 Avenue of the Americas

;; CITY: New York

;; STATE: NY

;; COUNTRY: USA

;; ZIP: 10036-2811

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: DOS

;; SOFTWARE: FastSEQ Version 2.0

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/10/283,599

;; FILING DATE: 29-OCT-2002

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/940,136

;; FILING DATE: 29-SEP-1997

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Coruzzi, Laura A

;; REGISTRATION NUMBER: 30,742

;; REFERENCE/DOCKET NUMBER: 009196-0007-999

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 650-493-4935

;; TELEFAX: 650-493-5556

;; TELEX: 66141 PENNIE

;; INFORMATION FOR SEQ ID NO: 242:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 18 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: No. 6844327e

;; US-10-283-599-242

Query Match 79.6%; Score 78; DB 2; Length 18;

Best Local Similarity 72.2%; Pred.No. 1.1e-05;

Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRPIRAFVG 18

||:|||||:|:|

Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 15

US-09-465-718-242

;; Sequence 242, Application US/09465718

;; Patent No. 6900177

;; GENERAL INFORMATION:

;; APPLICANT: Dasseux, Jean-Louis

;; APPLICANT: Sekul, Renate

;; APPLICANT: Buttner, Klaus

;; APPLICANT: Cornut, Isabelle

;; APPLICANT: Metz, Gunther

;; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

;; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

;; NUMBER OF SEQUENCES: 258

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Pennie & Edmonds LLP

;; STREET: 1155 Avenue of the Americas

;; CITY: New York

;; STATE: NY

;; COUNTRY: USA

;; ZIP: 10036-2811

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: DOS

;; SOFTWARE: FastSEQ Version 2.0

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/465,718

;; FILING DATE: 17-Dec-1999

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US/08/940,096

;; FILING DATE: 29-SEP-1997

;; APPLICATION NUMBER:

;; FILING DATE:

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Coruzzi, Laura A

;; REGISTRATION NUMBER: 30,742

;; REFERENCE/DOCKET NUMBER: 009196-0005-999

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 650-493-4935

;; TELEFAX: 650-493-5556

;; TELEX: 66141 PENNIE

;; INFORMATION FOR SEQ ID NO: 242:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 18 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: No. 6900177e

;; US-09-465-718-242

Query Match 79.6%; Score 78; DB 2; Length 18;

Best Local Similarity 72.2%; Pred.No. 1.1e-05;

Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRPIRAFVG 18

||:|||||:|:|

Db 1 GIKKFLGSIWKFIKAFVG 18

Search completed: May 19, 2006, 14:42:56

Job time : 25.8571 secs

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 15:18:19 ; Search time 81.2857 seconds
(without alignments)
102.575 Million cell updates/sec

Title: US-10-712-447-10

Perfect score: 98

Sequence: 1 GIRFLGSIWRFIRAFVG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pbp.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pbp.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pbp.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_PUBCOMB.pbp.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pbp.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pbp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	18	4	US-10-712-447-2
2	98	100.0	18	4	US-10-712-447-5
3	98	100.0	18	4	US-10-712-447-8
4	98	100.0	18	4	US-10-712-447-10
5	98	100.0	18	4	US-10-712-447-13
6	95	96.9	18	4	US-10-712-447-31
7	94	95.9	18	4	US-10-712-447-115
8	94	95.9	18	4	US-10-712-447-116
9	94	95.9	18	4	US-10-712-447-129
10	94	95.9	18	4	US-10-712-447-129
11	94	95.9	18	4	US-10-712-447-131
12	92	93.9	18	4	US-10-712-447-21
13	92	93.9	18	4	US-10-712-447-53
14	92	93.9	18	4	US-10-712-447-74
15	90	91.8	18	4	US-10-712-447-4
16	90	91.8	18	4	US-10-712-447-127
17	89	90.8	18	4	US-10-712-447-99
18	88	89.8	18	4	US-10-712-447-18
19	88	89.8	18	4	US-10-712-447-112
20	88	89.8	18	4	US-10-712-447-113
21	88	89.8	18	4	US-10-712-447-114
22	87	88.8	18	4	US-10-712-447-17
23	86	87.8	18	4	US-10-712-447-61
24	86	87.8	18	4	US-10-712-447-81
25	85	86.7	18	4	US-10-712-447-16
26	85	86.7	18	4	US-10-712-447-96
27	85	86.7	18	4	US-10-712-447-121

28	84	85.7	18	4	US-10-712-447-22	Sequence 22, Appl
29	84	85.7	18	4	US-10-712-447-78	Sequence 78, Appl
30	84	85.7	18	4	US-10-712-447-95	Sequence 95, Appl
31	84	85.7	18	4	US-10-712-447-120	Sequence 120, Appl
32	82	83.7	18	4	US-10-712-447-19	Sequence 19, Appl
33	82	83.7	18	4	US-10-712-447-56	Sequence 56, Appl
34	82	83.7	18	4	US-10-712-447-58	Sequence 58, Appl
35	82	83.7	18	4	US-10-712-447-77	Sequence 77, Appl
36	82	83.7	18	4	US-10-712-447-79	Sequence 80, Appl
37	82	83.7	18	4	US-10-712-447-80	Sequence 94, Appl
38	82	83.7	18	4	US-10-712-447-94	Sequence 57, Appl
39	81	82.7	18	4	US-10-712-447-57	Sequence 100, Appl
40	81	82.7	18	4	US-10-712-447-100	Sequence 97, Appl
41	80	81.6	18	4	US-10-712-447-41	Sequence 242, Appl
42	79	80.6	18	4	US-10-712-447-97	Sequence 242, Appl
43	78	79.6	18	3	US-09-865-989-242	Sequence 242, Appl
44	78	79.6	18	3	US-09-865-989-242	Sequence 242, Appl
45	78	79.6	18	4	US-10-099-574A-242	Sequence 242, Appl

ALIGNMENTS

RESULT 1
US-10-712-447-2
; Sequence 2, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712.447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; OTHER INFORMATION: c-term amidated
US-10-712-447-2
Query Match 100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;
Oy 1 GIRFLGSIWRFIRAFYG 18
Db 1 GIRFLGSIWRFIRAFYG 18
RESULT 2
US-10-712-447-5
; Sequence 5, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712.447
; CURRENT FILING DATE: 2003-11-13

```
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-5

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18
Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 3
US-10-712-447-8
; Sequence 8, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-8

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18
Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 4
US-10-712-447-10
; Sequence 10, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-10

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18
Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 5
US-10-712-447-13
; Sequence 13, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-13

Query Match      100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18
Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 6
US-10-712-447-91
; Sequence 91, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 91
; LENGTH: 18
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; US-10-712-447-91

Query Match          96.9%; Score 95; DB 4; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.8e-07;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFYG 18
   ||:|||||
Db 1 GIRKFLGSIWRFIRAFYG 18
   ||:|||||

RESULT 7
US-10-712-447-115
; Sequence 115, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 115
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; US-10-712-447-115

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFYG 18
   ||:|||||
Db 1 GLRRFIGSIWRFIRAFYG 18
   ||:|||||

RESULT 8
US-10-712-447-116
; Sequence 116, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 116
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; US-10-712-447-116
```

```
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; US-10-712-447-116

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFYG 18
   ||:|||||
Db 1 GLRRFIGSIWRFIRAFYG 18
   ||:|||||

RESULT 9
US-10-712-447-117
; Sequence 117, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 117
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; US-10-712-447-117

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFYG 18
   ||:|||||
Db 1 GIRRFIGSIWRFIRAFYG 18
   ||:|||||

RESULT 10
US-10-712-447-129
; Sequence 129, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 129
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; US-10-712-447-129
```

```
Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18
   |||||:||||:||||
Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 11
US-10-712-447-131
; Sequence 131, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 131
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-131

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18
   |||||:||||:||||
Db 1 GLRFLGSIWRFIRAFYG 18

RESULT 12
US-10-712-447-21
; Sequence 21, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 21
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-21

Query Match          93.9%; Score 92; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 7.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18
   |||||:||||:||||
Db 1 GIRRFLGAIWRFIRSFYG 18

RESULT 13
US-10-712-447-53
; Sequence 53, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 53
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; NAME/KEY: MOD RES
; LOCATION: (3)
; OTHER INFORMATION: (DiMe)Lys
; NAME/KEY: MOD RES
; LOCATION: (14)
; OTHER INFORMATION: (DiMe)Lys
US-10-712-447-53

Query Match          93.9%; Score 92; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 7.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18
   |||||:||||:||||
Db 1 GIKRFLGSIWRFIRAFYG 18

RESULT 14
US-10-712-447-74
; Sequence 74, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 74
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
```

```
; OTHER INFORMATION: peptide
US-10-712-447-74
Query Match      93.9%; Score 92; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 7.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GIRRFLGSIWRFIRAFYG 18
      |||:|||||:|||||
Db      1 GIRKFLGSIWRFIRAFYG 18

RESULT 15
US-10-712-447-4
; Sequence 4, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712.447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-4
Query Match      91.8%; Score 90; DB 4; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.6e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GIRRFLGSIWRFIRAFYG 18
      |||:|||||:|||||
Db      1 GIRRFLGSIWRFIRAFYG 18

Search completed: May 19, 2006, 15:27:57
Job time : 81.2857 secs
```

This Page Blank (uspto)


```
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; TITLE OF INVENTION: 14395, 14618, 17692, 58674, 252, 304, 1980, 14717, 9941, 19310,
; FILE REFERENCE: MPI2001-288PIRCPIONNM
; CURRENT APPLICATION NUMBER: US/11/242.505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290, 078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347, 949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320, 351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341, 606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-242-505A-18

Query Match      37.8%; Score 37; DB 7; Length 403;
Best Local Similarity 55.6%; Pred. No. 16;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      2 IRPFLGSIW 10
Db      155 VRRVLGAV 163

RESULT 3
US-09-949-925-142
; Sequence 142, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 142
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (60)
; OTHER INFORMATION: Xaa equals stop translation
US-09-949-925-142
```

```
Query Match      37.2%; Score 36.5; DB 1; Length 60;
Best Local Similarity 57.1%; Pred. No. 2.2;
Matches 8; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy      5 FLGSIWRFIRAFYG 18
Db      31 FLILVWIFV-AFYG 43

RESULT 4
US-09-949-925-111
; Sequence 111, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (74)
; OTHER INFORMATION: Xaa equals stop translation
US-09-949-925-111

Query Match      36.7%; Score 36; DB 1; Length 74;
Best Local Similarity 54.5%; Pred. No. 3.3;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      2 IRFLGSIWRF 12
Db      59 LREVSGKIWRF 69

RESULT 5
US-11-302-678-5
; Sequence 5, Application US/11302678
; Publication No. US2006008881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MPI02-012PIRNM_OMNI
```

Db 195 LEEAWSFDAFY 206

RESULT 7

US-10-511-937-2540

; Sequence 2540, Application US/10511937

; Publication No. US20060088836A1

; GENERAL INFORMATION:

; APPLICANT: EXPRESSION DIAGNOSTICS, INC.

; APPLICANT: Wohlseumuth, Jay

; APPLICANT: Fry, Kirk

; APPLICANT: Woodward, Robert

; APPLICANT: Ly, Ngoc

; APPLICANT: Prentice, James

; APPLICANT: Morris, MacDonald

; APPLICANT: Rosenberg, Steven

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION

; FILE REFERENCE: 506612000104

; CURRENT APPLICATION NUMBER: US/10/511.937

; CURRENT FILING DATE: 2004-10-19

; PRIOR APPLICATION NUMBER: PCT/US2003/012946

; PRIOR FILING DATE: 2003-04-24

; PRIOR APPLICATION NUMBER: US 10/131,831

; PRIOR FILING DATE: 2002-04-24

; PRIOR APPLICATION NUMBER: US 10/325,899

; PRIOR FILING DATE: 2002-12-20

; NUMBER OF SEQ ID NOS: 3117

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 2540

; LENGTH: 351

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-511-937-2540

Query Match 36.7%; Score 36; DB 7; Length 599;

Best Local Similarity 71.4%; Pred. No. 38;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LGSIWRF 12

Db 64 LGNVWRF 70

RESULT 6

US-11-242-505A-48

; Sequence 48, Application US/11242505A

; Publication No. US20060099656A1

; GENERAL INFORMATION:

; APPLICANT: Carroll, Joseph M.

; APPLICANT: Healy, Aileen

; TITLE OF INVENTION: Methods and Compositions for Treating

; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,

; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,

; FILE REFERENCE: MPI2001-288P10NNIM

; CURRENT APPLICATION NUMBER: US/11/242.505A

; CURRENT FILING DATE: 2005-10-03

; PRIOR APPLICATION NUMBER: US 10/290, 078

; PRIOR FILING DATE: 2002-11-07

; PRIOR APPLICATION NUMBER: US 60/347, 949

; PRIOR FILING DATE: 2001-11-07

; PRIOR APPLICATION NUMBER: US 10/320, 351

; PRIOR FILING DATE: 2002-12-16

; PRIOR APPLICATION NUMBER: 60/341, 606

; PRIOR FILING DATE: 2001-12-17

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 48

; LENGTH: 313

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-242-505A-48

Query Match 34.7%; Score 34; DB 7; Length 313;

Best Local Similarity 50.0%; Pred. No. 39;

Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 6 LGSIWRF 17

Query Match 34.7%; Score 34; DB 6; Length 351;

Best Local Similarity 46.2%; Pred. No. 44;

Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 6 LGSIWRF 18

Db 263 LGTVLKMFLFYG 275

RESULT 8

US-10-975-692-2

; Sequence 2, Application US/10975692

; Publication No. US20060090221A1

; GENERAL INFORMATION:

; APPLICANT: WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION

; APPLICANT: Browne, John A

; APPLICANT: Watts, James G

; APPLICANT: Wallis, Jennifer L.

; TITLE OF INVENTION: DESATURASES AND METHODS OF USING THEM FOR SYNTHESIS OF

; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS

; FILE REFERENCE: 4630-58963-02

; CURRENT APPLICATION NUMBER: US/10/975.693

; CURRENT FILING DATE: 2004-10-26

; PRIOR APPLICATION NUMBER: US 09/857, 583

; PRIOR FILING DATE: 2001-08-17

; PRIOR APPLICATION NUMBER: PCT/US99/28655

; PRIOR FILING DATE: 1999-12-06

; PRIOR APPLICATION NUMBER: US 60/111,301

; PRIOR FILING DATE: 1998-12-07

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: Patent in version 3.3

; SEQ ID NO 2

; LENGTH: 447

; TYPE: PRT

; ORGANISM: Caenorhabditis elegans

US-10-975-692-2

Query Match 34.7%; Score 34; DB 6; Length 447;
Best Local Similarity 43.8%; Pred. No. 59;
Matches 7; Conservative 4; Mismatches 5; Indels

QY 2 IRRELGSIWRFIRAFY 17
||: ||: : ||
Db 130 IRKILETIFTILFAFY 145

```

RESULT 9
US-10-505-928-543
; Sequence 543, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 543
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-543

```

Query Match 34.7%; Score 34; DB 6; Length 522;
Best Local Similarity 47.1%; Pred. No. 70;
Matches 8; Conservative 3; Mismatches 4; Indels

Qy 3 RRFL--GSIWRFIRAFY 17
 ||| | : | | | :
 Db 473 RRFTOSGDLYRHIRKFH 489

RESULT 10
 US-11-169-140-109
 ; Sequence 109, Application US/11169140
 ; Publication No. US20060099150A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
 ; APPLICANT: HOUSTON, Lou, L.
 ; APPLICANT: SHERIDAN, Philip, J.
 ; APPLICANT: HAWLEY, Stephen
 ; APPLICANT: GYNN, Jacqueline, M.
 ; APPLICANT: CHAPIN, Steven
 ; TITLE OF INVENTION: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CELL
 ; TITLE OF INVENTION: BARRIERS
 ; FILE REFERENCE: 11474-037-999
 ; CURRENT APPLICATION NUMBER: US/11/169,140
 ; CURRENT FILING DATE: 2005-06-27, 601
 ; PRIOR APPLICATION NUMBER: US 60/267,601
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: US 60/248,819
 ; PRIOR FILING DATE: 2000-11-14
 ; PRIOR APPLICATION NUMBER: US 60/248,478
 ; PRIOR FILING DATE: 2000-11-13
 ; PRIOR APPLICATION NUMBER: US 60/237,929
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: 09/949,039
 ; PRIOR FILING DATE: 2001-09-06
 ; PRIOR APPLICATION NUMBER: 09/969,748
 ; PRIOR FILING DATE: 2001-10-02
 ; NUMBER OF SEQ ID NOS: 143
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 109
 ; LENGTH: 244
 ; TYPE: PRT
 ; ORGANISM: Simian
 US-11-169-140-109

Query Match 34.2%; Score 33.5; DB 7; Length 244;
Best Local Similarity 42.1%; Pred. No. 35;
Matches 8; Conservative 3; Mismatches 3; Indels

```

Qy      1 GIRRFLGSIW-----RFIR 14
         | : | | : | | |
Db     158 GLVLALGAVWCVARARFIR 176

```

```

RESULT 11
US-11-204-427-7
; Sequence 7, Application US/11204427
; Publication No. US20080100146A1
; GENERAL INFORMATION:
; APPLICANT: Sturley, Stephen L
; APPLICANT: Turkish, Aaron R
; APPLICANT: Billheimer, Jeffrey T
; APPLICANT: Cromley, Debra
; TITLE OF INVENTION: AWAT-RELATED METHODS AND ARTICLES
; FILE REFERENCE: 0575/72796/JPW/AJM/JCS
; CURRENT APPLICATION NUMBER: US/11/204, 427
; CURRENT FILING DATE: 2005-08-15
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-204-427-7

```

Query Match 33.7%; Score 33; DB 7; Length 342;
Best Local Similarity 50.0%; Pred. No. 63;
Matches 5; Conservative 3; Mismatches 2; Indels

Qy	8 SIWRFIRAFY 17
	: : : : :
Db	84 AIWROLRDY 93

```

RESULT 12
US-11-304-129-40
; Sequence 40, Application US/11304129
; Publication No. US2006008915A1
; GENERAL INFORMATION:
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: WASUDA, Yasushi
; APPLICANT: TAKATSU, Yoshihiro
; APPLICANT: WATANABE, Takuya
; APPLICANT: TERAO, Yasuko
; APPLICANT: SHINTANI, Yasushi
; APPLICANT: HINUMA, Syuji
; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
; FILE REFERENCE: 2762US0P
; CURRENT APPLICATION NUMBER: US/11/304,129
; CURRENT FILING DATE: 2005-12-15
; PRIOR APPLICATION NUMBER: US/10/333,192
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: JP 2000-217442
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: JP 2001-26779
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/JP01/06162
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 40
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Rat
US-11-304-129-40

Query Match          33.7%;   Score 33;   DB 7;   Length 393;
Best Local Similarity 46.2%;   Pred. No. 75;

```

Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 FLGSIWRFIRAFY 17

Db 216 FCGIWPVDQIFY 228

RESULT 13

US-11-304-129-48
; Sequence 48, Application US/11304129
; Publication No. US2006008915A1
; GENERAL INFORMATION:
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: TAKATSU, Yoshihiro
; APPLICANT: WATANABE, Takuya
; APPLICANT: TERAU, Yasuko
; APPLICANT: SHINTANI, Yasushi
; APPLICANT: HINUMA, Syuji
; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
; FILE REFERENCE: 2762USOP
; CURRENT APPLICATION NUMBER: US/11/304,129
; CURRENT FILING DATE: 2005-12-15
; PRIOR APPLICATION NUMBER: US/10/333,192
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: JP 2000-217442
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: JP 2001-26779
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/JP01/06162
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 48
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Mouse
US-11-304-129-48

Query Match 33.7%; Score 33; DB 7; Length 393;
Best Local Similarity 46.2%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 FLGSIWRFIRAFY 17

Db 216 FCGIWPVDQIFY 228

RESULT 14

US-10-505-928-545
; Sequence 545, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 545
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-545

Query Match 33.7%; Score 33; DB 6; Length 463;
Best Local Similarity 33.3%; Pred. No. 90;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 4 RFLGSIWRFIRAFY 18

| : | : |

Db 339 RYYSBYHYVGGFY 353

RESULT 15

US-10-505-928-853
; Sequence 853, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 853
; LENGTH: 1531
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-853

Query Match 33.7%; Score 33; DB 6; Length 1531;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 LGSIWRFIRAFY 17

Db 1122 LGLIYFVQRFY 1133

Search completed: May 19, 2006, 15:28:18
Job time : 2.14286 secs

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:13:22 ; Search time 94.2857 Seconds
(without alignments)

87.287 Million cell updates/sec

Title: US-10-712-447-13

Perfect score: 98

Sequence: 1 GRRFLGSIWRFIRAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_8.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*
- 10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	18	ADO34231	Ado34231 Synthetic
2	98	100.0	18	ADO34225	Ado34225 Synthetic
3	98	100.0	18	ADO34228	Ado34228 Synthetic
4	98	100.0	18	ADO34236	Ado34236 Synthetic
5	98	100.0	18	ADO34233	Ado34233 Synthetic
6	95	95.9	18	ADO34314	Ado34314 Synthetic
7	94	95.9	18	ADO34354	Ado34354 Synthetic
8	94	95.9	18	ADO34338	Ado34338 Synthetic
9	94	95.9	18	ADO34352	Ado34352 Synthetic
10	94	95.9	18	ADO34340	Ado34340 Synthetic
11	94	95.9	18	ADO34339	Ado34339 Synthetic
12	92	93.9	18	ADO34297	Ado34297 Synthetic
13	92	93.9	18	ADO34244	Ado34244 Synthetic
14	92	93.9	18	ADO34276	Ado34276 Synthetic
15	90	91.8	18	ADO34227	Ado34227 Synthetic
16	90	91.8	18	ADO34350	Ado34350 Synthetic
17	89	90.8	18	ADO34322	Ado34322 Synthetic
18	88	89.8	18	ADO34336	Ado34336 Synthetic
19	88	89.8	18	ADO34335	Ado34335 Synthetic
20	88	89.8	18	ADO34337	Ado34337 Synthetic
21	88	89.8	18	ADO34241	Ado34241 Synthetic
22	87	88.8	18	ADO34240	Ado34240 Synthetic
23	86	87.8	18	ADO34284	Ado34284 Synthetic

24	86	87.8	18	ADO34305	Ado34305 Synthetic
25	85	86.7	18	ADO34239	Ado34239 Synthetic
26	85	86.7	18	ADO34344	Ado34344 Synthetic
27	85	86.7	18	ADO34319	Ado34319 Synthetic
28	84	85.7	18	ADO34245	Ado34245 Synthetic
29	84	85.7	18	ADO34301	Ado34301 Synthetic
30	84	85.7	18	ADO34343	Ado34343 Synthetic
31	84	85.7	18	ADO34318	Ado34318 Synthetic
32	82	83.7	18	ADO34302	Ado34302 Synthetic
33	82	83.7	18	ADO34279	Ado34279 Synthetic
34	82	83.7	18	ADO34303	Ado34303 Synthetic
35	82	83.7	18	ADO34242	Ado34242 Synthetic
36	82	83.7	18	ADO34300	Ado34300 Synthetic
37	82	83.7	18	ADO34281	Ado34281 Synthetic
38	82	83.7	18	ADO34317	Ado34317 Synthetic
39	81	82.7	18	ADO34323	Ado34323 Synthetic
40	81	82.7	18	ADO34280	Ado34280 Synthetic
41	80	81.6	18	ADO34264	Ado34264 Synthetic
42	79	80.6	18	ADO34320	Ado34320 Synthetic
43	78	79.6	18	AAI18917	Aay18917 Lecithin:
44	78	79.6	18	AAI19171	Aay19171 Lecithin:
45	78	79.6	18	AAI19425	Aay19425 Lecithin:

ALIGNMENTS

RESULT 1

ADO34231
ID ADO34231 standard; peptide; 18 AA.

XX AC ADO34231;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 8.

XX KW apolipoprotein-E mimicking polypeptide; antilipemic; cardiatic;
KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
coronary artery disease, dysbetalipoproteinemia or atherosclerosis
comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 8; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking
polypeptide. The invention further comprises an isolated nucleic acid
encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
a host cell, a recombinant cell or a transgenic, non-human subject
(including animal or plant) comprising the synthetic apolipoprotein-E
mimicking polypeptide encoding polynucleotide; a composition comprising
the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipemic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianigmal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFIRAFYG 18
 |||||
 Db 1 GIRRFGLSIWRFIRAFYG 18
 |||||

RESULT 2
 ADO34225
 ID ADO34225 standard; peptide; 18 AA.
 XX ADO34225;
 AC ADO34225;
 XX 12-AUG-2004 (first entry)
 DT Synthetic apolipoprotein-E mimicking polypeptide related R18L peptide.
 DE
 XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianigmal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 1 /notes= "N-terminal acetyl"
 FT Modified-site 18 /notes= "C-terminal amide"
 FT
 XX WO2004043403-A2.
 PN
 XX 27-MAY-2004.
 PD
 XX 13-NOV-2003; 2003WO-US036268.
 PF
 XX 13-NOV-2002; 2002US-0425821P.
 PR
 XX (UABR-) UAB RES FOUND.
 PA
 XX Anantharamiah GM, Garber DW, Datta G;
 PI WPI; 2004-411629/38.
 DR
 XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 XX coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 XX comprises an amino acid sequence.
 XX
 XX Claim 4; SEQ ID NO 2; 79pp; English.
 PS
 XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,

CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipemic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianigmal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFIRAFYG 18
 |||||
 Db 1 GIRRFGLSIWRFIRAFYG 18
 |||||

RESULT 3
 ADO34228
 ID ADO34228 standard; peptide; 18 AA.
 XX ADO34228;
 AC ADO34228;
 XX 12-AUG-2004 (first entry)
 DT Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 5.
 DE
 XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianigmal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
 XX Synthetic.
 OS
 XX WO2004043403-A2.
 PN
 XX 27-MAY-2004.
 PD
 XX 13-NOV-2003; 2003WO-US036268.
 PF
 XX 13-NOV-2002; 2002US-0425821P.
 PR
 XX (UABR-) UAB RES FOUND.
 PA
 XX Anantharamiah GM, Garber DW, Datta G;
 PI WPI; 2004-411629/38.
 DR
 XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 XX coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 XX comprises an amino acid sequence.
 XX
 XX Claim 4; SEQ ID NO 5; 79pp; English.
 PS
 XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,

CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRIFIRAFYG 18
 |||||
 Db 1 GIRRFLGSIWRIFIRAFYG 18

RESULT 4
 ADO34236
 ID ADO34236 standard; peptide; 18 AA.

AC ADO34236;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 13.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 13; 79pp; English.

CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E

CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRIFIRAFYG 18
 |||||
 Db 1 GIRRFLGSIWRIFIRAFYG 18

RESULT 5
 ADO34233
 ID ADO34233 standard; peptide; 18 AA.

AC ADO34233;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 10.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 10; 79pp; English.

CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising

CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipemic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.
 XX
 SQ Sequence 18 AA;
 Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GIRRFGLSIWRFIRAFYG 18
 |||||
 Db 1 GIRRFGLSIWRFIRAFYG 18
 |||||
 RESULT 6
 ADO34314
 ID ADO34314 standard; peptide; 18 AA.
 XX
 AC ADO34314;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 91.
 XX
 KW apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
 XX
 OS Synthetic.
 XX
 FN WO2004043403-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 13-NOV-2003; 2003WO-US036268.
 XX
 PR 13-NOV-2002; 2002US-0425821P.
 XX
 PA (UABR-) UAB RES FOUND.
 XX
 PI Anantharamiah GM, Garber DW, Datta G;
 XX
 DR WPI; 2004-411629/38.
 XX
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.
 XX
 PS Claim 4; SEQ ID NO 91; 79pp; English.
 XX
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipemic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.
 XX
 SQ Sequence 18 AA;
 Query Match 96.9%; Score 95; DB 8; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.8e-07;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GIRRFGLSIWRFIRAFYG 18
 |||||
 Db 1 GIRRFGLSIWRFIRAFYG 18
 |||||
 RESULT 7
 ADO34354
 ID ADO34354 standard; peptide; 18 AA.
 XX
 AC ADO34354;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 131.
 XX
 KW apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
 XX
 OS Synthetic.
 XX
 FN WO2004043403-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 13-NOV-2003; 2003WO-US036268.
 XX
 PR 13-NOV-2002; 2002US-0425821P.
 XX
 PA (UABR-) UAB RES FOUND.
 XX
 PI Anantharamiah GM, Garber DW, Datta G;
 XX
 DR WPI; 2004-411629/38.
 XX
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.
 XX
 PS Claim 4; SEQ ID NO 131; 79pp; English.
 XX
 CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18
 |:|||||:|||||
 Db 1 GLRRFLGSIWRFIRAFYG 18

RESULT 8
 ADO34338
 ID ADO34338 standard; peptide; 18 AA.

XX AC ADO34338;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 115.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX FN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 115; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18
 |:|||||:|||||
 Db 1 GLRRFLGSIWRFIRAFYG 18

RESULT 9
 ADO34352
 ID ADO34352 standard; peptide; 18 AA.

XX AC ADO34352;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 129.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX FN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 129; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,

CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18
 |||||:||||:||||
 Db 1 GIRRFLGSLWRFIRAFYG 18

RESULT 10

ADO34340
 ID ADO34340 standard; peptide; 18 AA.

XX ADO34340;

XX 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 117.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 117; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYG 18

Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 11

ADO34339

ID ADO34339 standard; peptide; 18 AA.

XX ADO34339;

XX 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 116.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 116; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector comprising the synthetic apolipoprotein-E mimicking polypeptide; a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and a monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipemic, cardiatic, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,

CC chimpanzee or orangutan); for treating coronary artery disease.
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 93.9%; Score 92; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 5.3e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYVG 18
 |||:||||:||||:||||
 Db 1 GIRRFLGAIWRFIRSFYVG 18

RESULT 14

ADO34276
 ID ADO34276 standard; peptide; 18 AA.

AC ADO34276;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 53.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1.18 /note= "All Lys residues are DiMethyl-Lysine"

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 53; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipemic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 93.9%; Score 92; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 5.3e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFYVG 18
 |||:||||:||||:||||
 Db 1 GIKRFLGSIWRFIRAFYVG 18

RESULT 15

ADO34227
 ID ADO34227 standard; peptide; 18 AA.

AC ADO34227;

XX 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking related R18L linear peptide.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 4; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipemic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

CC useful for reducing serum cholesterol in a subject (including a mammal
CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
CC chimpanzee or orangutan); for treating coronary artery disease,
CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
CC myocardial infarction or stroke; for breaking an embolus in the subject;
CC and also for treating angina. The synthetic apolipoprotein-E mimicking
CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
CC mimicking polypeptide of the invention.

XX

SQ Sequence 18 AA;

Query Match 91.8%; Score 90; DB 8; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.1e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFVG 18

|||||

Db 1 GIRRFLGSIWRFIRAFVG 18

Search completed: May 19, 2006, 14:24:30
Job time : 95.2857 secs

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:24:57 ; Search time 14.2857 Seconds
(without alignments)
121.233 Million cell updates/sec

Title: US-10-712-447-13
Perfect score: 98
Sequence: 1 GIRRFGLSIWRFIRAFYG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	49.0	627	S76462	hypothetical prote
2	45	45.9	178	A75578	transcription regu
3	44	44.9	461	G64537	2-oxoglutarate/mal
4	44	44.9	589	A34341	poly(3-hydroxybuty
5	44	44.9	806	A84060	leucyl-tRNA synthet
6	44	44.9	861	H64102	leucine-tRNA ligas
7	43.5	44.4	1025	AH3568	acridine resistanc
8	43	43.9	265	T23236	hypothetical prote
9	43	43.9	489	B84733	probable cytochrom
10	43	43.9	516	T33269	hypothetical prote
11	43	43.9	812	A46417	NIP1 protein - yea
12	43	43.9	1607	T04583	TMV resistance pro
13	42.5	43.4	407	T12085	reverse transcript
14	42.5	43.4	760	E84953	penicillin-binding
15	42	42.9	107	T52113	probable transcrip
16	42	42.9	214	D72540	hypothetical prote
17	42	42.9	228	T15530	hypothetical prote
18	42	42.9	237	B72692	hypothetical prote
19	42	42.9	246	I54412	MHC HLA-A cell sur
20	42	42.9	258	F71707	o-antigen export s
21	42	42.9	258	D97700	o-antigen export s
22	42	42.9	273	HLH069	MHC class I histoc
23	42	42.9	365	HLH042	MHC class I histoc
24	42	42.9	365	I38443	Gene HLA-A-0203 pr
25	42	42.9	365	I61902	MHC class I histoc
26	42	42.9	365	I37542	MHC class I histoc
27	42	42.9	365	I84448	MHC class I histoc
28	42	42.9	365	I61857	MHC HLA-A2.4a chai
29	42	42.9	365	I38442	gene HLA-A-0205 pr

Query Match 45.9% ; Score 45; DB 2; Length 178;

ALIGNMENTS

RESULT 1

S76462
hypothetical protein - Synchocystis sp. (strain PCC 6803)
C:Species: Synchocystis sp.

A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S76462

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis
s.

A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76462
A>Status: preliminary
A:Molecule type: DNA

A:Residues: 1-627 <KAN>
A:Cross-references: UNIPROT:P74489; UNIPARC:UPI00000C103F; EMBL:D90915; GB:AB001339; NID:
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 49.0% ; Score 48; DB 2; Length 627;
Best Local Similarity 38.9% ; Pred. No. 8.1;
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GIRRFGLSIWRFIRAFYG 18
Db 597 GLEQLLEKIQWLKQKFG 614

RESULT 2

A75578
transcription regulator, MarR family - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: A75578
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: A75578
A>Status: preliminary

A:Molecule type: DNA
A:Residues: 1-178 <WHI>

A:Cross-references: UNIPROT:Q9RYR0; UNIPARC:UPI00000D3BE4; GB:AE001863; GB:AE001825; NID:
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRA0248
A:Map position: 2

Query Match 45.9% ; Score 45; DB 2; Length 178;

Best Local Similarity 69.2%; Pred. No. 7.2;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 IRRFLGSIWRFIR 14
| | | | |
Db 23 ILRFLGGIWRLLNR 35

RESULT 3
G64537
2-oxoglutarate/malate translocator - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: G64537
R:Tomb, J.F.; White, O.; Kervilavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne-son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:9739467; PMID:9252185
A:Accession: G64537
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-461 <TOM>
A:Cross-references: UNIPARC:UPI0000174217; GB:AE000511; TIGR:HP0143
C:Superfamily: 2-oxoglutarate/malate translocator

Query Match 44.9%; Score 44; DB 1; Length 461;
Best Local Similarity 53.8%; Pred. No. 26;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IRRFLGSIWRFIR 14
: | | | | |
Db 297 VRLLSFWFWRVR 309

RESULT 4
A34341
poly(3-hydroxybutyrate) synthase (EC 2.3.1.-) - Alcaligenes eutrophus
C:Species: Alcaligenes eutrophus
C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C:Accession: A34341; A39190
R:Peoples, O.P.; Sinskey, A.J.
J. Biol. Chem. 264, 15298-15303, 1989
A:Title: Poly-beta-hydroxybutyrate (PHB) biosynthesis in Alcaligenes eutrophus H16. Ident
A:Reference number: A34341; MUID:89359357; PMID:2670936
A:Accession: A34341
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-589 <PEO>
A:Cross-references: UNIPROT:P23608; UNIPARC:UPI0000044953; GB:J05003; NID:g141958; PIDN:
R:Schubert, P.; Krueger, N.; Steinbuechel, A.
J. Bacteriol. 173, 168-175, 1991
A:Title: Molecular analysis of the Alcaligenes eutrophus poly(3-hydroxybutyrate) biosynth
omoter.
A:Reference number: A39190; MUID:91100279; PMID:1987116
A:Accession: A39190
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-219 <SCH>
A:Cross-references: UNIPARC:UPI000015E162; GB:M64341; NID:g141964; PIDN:AAA21979.1; PID:
A:Note: the authors translated the codon TAC for residue 120 as Thr
C:Superfamily: poly(3-hydroxyalkanoic acid) synthase phbc
C:Keywords: acyltransferase

Query Match 44.9%; Score 44; DB 2; Length 589;
Best Local Similarity 47.8%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

QY 3 RREFLGSIW-----RIFRIFY 17
| | | | |

Db 100 RRFAGDAWRTNLPYRFAPAFY 120

RESULT 5
A84060
leucyl-tRNA synthetase leuS [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: A84060
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: A84060
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-806 <STO>
A:Cross-references: UNIPROT:Q9K788; UNIPARC:UPI0000136555; GB:AP001518; GB:BA000004; NID:
A:Experimental source: strain C-125
C:Genetics:
A:Gene: leuS
C:Superfamily: leucine-tRNA ligase

Query Match 44.9%; Score 44; DB 2; Length 806;
Best Local Similarity 53.8%; Pred. No. 45;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFI 13
| | | | |
Db 622 GARRFLDRVWRLL 634

RESULT 6
H64102
leucine-tRNA ligase (EC 6.1.1.4) - Haemophilus influenzae (strain Rd KW20)
N:Alternate names: leucyl-tRNA synthetase
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C:Accession: H64102
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C.
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: H64102
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-861 <TIGR>
A:Cross-references: UNIPROT:P43827; UNIPARC:UPI000013655F; GB:U32774; GB:142023; NID:g157
C:Genetics:
A:Gene: leuS
C:Superfamily: leucine-tRNA ligase
C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 44.9%; Score 44; DB 2; Length 861;
Best Local Similarity 46.2%; Pred. No. 48;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFI 13
| | | | |
Db 665 GAKRFLGRVWNLV 677

RESULT 7
AH3568
acriflavin resistance protein F [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AH3568
R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova, I.
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
A;Reference number: AD3252; PMID:11756688
A;Accession: AH3568
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1025 <MUR>
A;Cross-references: UNIPROT:Q8YQC5; UNIPARC:UPI00000584C8; GB:AE008918; PIDN:AAU53715.1;
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI0473
A;Map position: II
C;Superfamily: hypothetical protein b2075

Query Match 44.4%; Score 43.5; DB 2; Length 1025;
Best Local Similarity 50.0%; Pred. No. 69;
Matches 8; Conservative 4; Mismatches 1; Indels 3; Gaps 1;

QY 5 FLGSIMRFI---RAFY 17
|||||:|:|:|:
Db 531 FLGSVWSFMTLPRSF 546

RESULT 8
T32316
hypothetical protein F31F4.4 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Dec-2004
C;Accession: T32316
R;Blanchard, M.; Kramer, J.; Elliott, G.; Twyman, B.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of *C. elegans* cosmid F31F4.
A;Reference number: Z21149
A;Accession: T32316
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-265 <BLA>
A;Cross-references: UNIPROT:O17136; UNIPARC:UPI000007D19A; EMBL:AF024503; PIDN:AAB70384.
A;Experimental source: strain Bristol N2; clone F31F4
C;Genetics:
A;Gene: CESP:F31F4.4
A;Map position: 5
A;Introns: 13/3; 67/2
C;Superfamily: *Caenorhabditis elegans* hypothetical protein T09F5.1

Query Match 43.9%; Score 43; DB 2; Length 265;
Best Local Similarity 53.8%; Pred. No. 22;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 LGSIMRFIRAFY 18
|||:|:|:|:
Db 253 LASLWAFVHAPEG 265

RESULT 9
B84733
probable cytochrome P450 [imported] - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B84733
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A;Reference number: B84420; MUID:20083487; PMID:10617197
A;Accession: B84733
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-489 <STO>
A;Cross-references: UNIPROT:Q9ZV72; UNIPARC:UPI000009D8ED; GB:AE002093; NID:G3831452; PI
C;Genetics:
A;Gene: At2g32440

A;Map position: 2
C;Superfamily: *Synechocystis* cytochrome P450 slr0574; cytochrome P450 homology

Query Match 43.9%; Score 43; DB 2; Length 489;
Best Local Similarity 54.5%; Pred. No. 40;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 LGSIMRFIRAF 16
|||:|:|:|:
Db 54 IGNMWSFLRAF 64

RESULT 10
T33269
hypothetical protein C24B9.13 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33269
R;Murray, J.; Wohlmann, P.; Langston, Y.; O'Neal, D.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of *C. elegans* cosmid C24B9.
A;Reference number: Z21310
A;Accession: T33269
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-516 <MUR>
A;Cross-references: UNIPROT:O76442; UNIPARC:UPI000007D477; EMBL:AF068709; PIDN:AAC19257.1;
A;Experimental source: strain Bristol N2; clone C24B9
C;Genetics:
A;Gene: CESP:C24B9.13
A;Map position: 5
A;Introns: 13/3; 67/2; 116/2; 268/2; 315/2; 364/2

Query Match 43.9%; Score 43; DB 2; Length 516;
Best Local Similarity 41.2%; Pred. No. 42;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 IRRFLSGIMRFIRAFY 18
|||:|:|:|:
Db 252 LKFFITSLWMFMHAFDG 268

RESULT 11
A46417
NIP1 protein - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: nuclear import protein; protein YM9924.01c; protein YM9952.11c; protei
C;Species: *Saccharomyces cerevisiae*
C;Date: 21-Sep-1993 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A46417; S53979; S59302
R;Gu, Z.; Moerscheil, R.P.; Sherman, F.; Goldfarb, D.S.
Proc. Natl. Acad. Sci. U.S.A. 89, 10355-10359, 1992
A;Title: NIP1, a gene required for nuclear transport in yeast.
A;Reference number: A46417; MUID:93066237; PMID:1332047
A;Accession: A46417
A;Molecule type: DNA
A;Residues: 1-812 <GUL>
A;Cross-references: UNIPROT:P32497; UNIPARC:UPI000017B2E1; EMBL:L02899
A;Note: sequence extracted from NCBI backbone (NCBIN:117849, NCBIIP:117850)
R;Connor, R.; Churcher, C.M.
submitted to the EMBL Data Library, April 1995
A;Reference number: S53969
A;Accession: S53979
A;Molecule type: DNA
A;Residues: 571-592, 'Q', 584-640, 'K', 642, 'K', 644-812 <CON>
A;Cross-references: UNIPARC:UPI0000168ACD; EMBL:Z49212; NID:G798940; PID:G798951; MIPS:YN
R;Churcher, C.M.
submitted to the EMBL Data Library, September 1995
A;Reference number: S59302
A;Accession: S59302
A;Molecule type: DNA
A;Residues: 1-110, 'V', 112-582, 'Q', 584-602 <CHU>
A;Cross-references: UNIPARC:UPI0000168ACA; EMBL:Z54141; NID:G1072408; PID:G984682; MIPS:YN
A;Experimental source: strain AB972

C;Genetics:

A;Gene: SGD:NIP1
A;Cross-references: SGD:S0004926; MIPS:YMR309C
A;Map position: 13R

Query Match 43.9%; Score 43; DB 2; Length 812;
Best Local Similarity 53.8%; Pred. No. 66;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 GIRFLGSIWRFI 13

||:|||||:
361 GVKRLGSIISFV 373

RESULT 12

T04583

TMV resistance protein N homolog F23E13.30 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: T04583; T05507

R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Dueterhoeft, A.; Jesse, T.

submitted to the Protein Sequence Database, March 1998

A;Reference number: T15378

A;Accession: T04583

A;Molecule type: DNA

A;Residues: 1-1607 <BEV>

A;Cross-references: UNIPROT:O65506; UNIPARC:UPI00000AA45C; EMBL:AL022141

A;Experimental source: cultivar Columbia; BAC clone F23E13

R;Bevan, M.; Wedler, H.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Schuelke

submitted to the Protein Sequence Database, April 1998

A;Reference number: T15418

A;Accession: T05507

A;Molecule type: DNA

A;Residues: 1448-1607 <BE2>

A;Cross-references: UNIPARC:UPI000016DBFD; EMBL:AL022373

A;Experimental source: cultivar Columbia; BAC clone T19K4

C;Genetics:

A;Map position: 4

A;Introns: 193/2; 238/2; 556/2; 930/3; 1029/3; 1287/3

A;Note: F23E13.30; T19K4.270

Query Match 43.9%; Score 43; DB 2; Length 1607;

Best Local Similarity 72.7%; Pred. No. 1.3e+02;

Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 LGSWRFIRAF 16

|||||||

Db 1321 LGSSWRLRGF 1331

RESULT 13

T12085

reverse transcriptase homolog - fava bean (fragment)

C;Species: Vicia faba (fava bean)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C;Accession: T12085

R;Kinoshita, T.; Wada, H.; Masaaki, I.; Shimazaki, K.

submitted to the EMBL Data Library, September 1997

A;Description: Retrotransposon-like cDNAs from guard cell protoplasts in Vicia faba.

A;Reference number: T17406

A;Accession: T12085

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-407 <KIN>

A;Cross-references: UNIPROT:O22103; UNIPARC:UPI00000AAD3D; EMBL:AB007466; NID:d1170509;

A;Experimental source: guard cell protoplasts

C;Superfamily: pol. polyprotein

Query Match

Best Local Similarity 43.4%; Score 42.5; DB 2; Length 407;

Matches 11; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

QY 1 GIRFLGSIW--RFIRAF 16

Db 178 GIRFLGHVGFRRFIRDF 196

|||||:|||||

RESULT 14

E84953

penicillin-binding protein 1b [imported] - Buchnera sp. (strain APS)

C;Species: Buchnera sp.

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002

C;Accession: E84953

R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.

Nature 407, 81-86, 2000

A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A1

A;Reference number: A84930; MUID:20445173; PMID:10993077

A;Accession: E84953

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-760 <STO>

A;Cross-references: UNIPARC:UPI000005E4C8; GB:AP000398; GSPDB:GN00144

A;Experimental source: strain APS

C;Genetics:

A;Gene: mrcB; BU200

C;Superfamily: penicillin-binding protein 1B

Query Match 43.4%; Score 42.5; DB 2; Length 760;

Best Local Similarity 44.4%; Pred. No. 74;

Matches 8; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

QY 2 IRRFLGSIWRFIRAFYG 18

||||:|||||

Db 32 INRFINGKWNPTSIYG 49

RESULT 15

T52113

probable transcription co-activator KIWI [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004

C;Accession: T52113

R;Cornack, R.S.; Hahlbrock, K.; Somssich, I.E.

Plant J. 14, 685-92, 1998

A;Title: Isolation of putative plant transcriptional coactivators using a modified two-hy

A;Reference number: Z25848; MUID:98346011; PMID:9681033

A;Accession: T52113

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-107 <COR>

A;Cross-references: UNIPROT:O65154; UNIPARC:UPI000000C45F; EMBL:AF053302; PIDN:AAC08574.1

A;Experimental source: cultivar Columbia

C;Genetics:

A;Gene: KIWI

A;Map position: V

C;Function:

A;Description: probably plays a role in gene activation during pathogen defence and plant

C;Superfamily: Caenorhabditis elegans hypothetical protein T13F2.2

Query Match 42.9%; Score 42; DB 2; Length 107;

Best Local Similarity 50.0%; Pred. No. 13;

Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 IRRFLGSIWRFIRAFY 17

||:|||||

Db 54 VRNNGKIWDIREFY 69

Search completed: May 19, 2006, 14:39:56

Job time : 18.2857 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:13:32 ; Search time 115.429 Seconds
(without alignments)
144.247 Million cell updates/sec

Title: US-10-712-447-13
Perfect score: 98
Sequence: 1 GIRRFLGSIWRFI AFYV 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues
Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	59.2	805	Q3APY5_CHLCH	Q3apY5 chlorobium
2	54	55.1	670	Q25271_LEPDE	Q25271 leptinotars
3	52	53.1	735	Q9F7V7_RHILV	Q9f7v7 rhizobium 1
4	52	53.1	805	Q44QD1_CHLLI	Q44qd1 chlorobium
5	52	53.1	816	Q43K01_9CHLB	Q43k01 chlorobium
6	51	52.0	407	Q39L57_BURK3	Q39l57 burkholderi
7	51	52.0	408	Q456F4_BURK	Q456f4 burkholderi
8	51	52.0	408	Q4LK44_BURK	Q4lk44 burkholderi
9	50	51.0	579	1_KXR7_HUMAN	Q5gh72 homo sapien
10	50	51.0	579	1_KXR7_PANTR	Q49l81 pan troglod
11	50	51.0	580	1_KXR7_MOUSE	Q5gh64 mus musculus
12	50	51.0	580	1_KXR7_RAT	Q5gh56 rattus norv
13	49	50.0	409	Q4BFM2_BURVI	Q4bfm2 burkholderi
14	49	50.0	449	Q3PK79_PARDE	Q3pk79 paracoccus
15	49	50.0	488	Q84ZM1_PEA	Q84zm1 pisum sativ
16	48	49.0	188	Q3ILN7_9DELT	Q3iln7 anaeromyxob
17	48	49.0	298	Q8R587_MOUSE	Q8r587 mus musculus
18	48	49.0	435	Q2JIT0_9CYAN	Q2jit0 cyanobacter
19	48	49.0	578	1_KXR6_TETNG	Q49l88 tetradodon n
20	48	49.0	578	Q5GH49_FUGRU	Q5gh49 fugu rubrip
21	48	49.0	627	Q74489_SYNY3	P74489 synecocyst
22	47.5	48.5	240	Q97035_HAESO	P97035 haemophilus
23	47.5	48.5	577	Q36XB4_RHOPA	Q36xb4 rhodospseudo
24	47.5	48.5	577	Q37C12_RHOPA	Q37cl2 rhodospseudo
25	47.5	48.5	807	Q3VMG0_9CHLB	Q3vmg0 pelodictyon
26	47	48.0	486	Q5U414_XENLA	Q5u414 xenopus lae
27	47	48.0	487	Q32N49_XENLA	Q32n49 xenopus lae
28	47	48.0	910	Q3ZDS6_ORYZA	Q5zds6 oryza sativ
29	46	46.9	361	Q2NUB5_SODGL	Q2nub5 sodalis glo
30	46	46.9	385	Q5ZPA2_9DELT	Q5zpa2 angiococcus
31	46	46.9	540	2_Q5GH65_MOUSE	Q5gh65 mus musculus

32	46	46.9	580	2	Q5GH40_BRAHE	Q5gh40 brachydanio
33	46	46.9	638	1	XKR6_RAT	Q5gh57 rattus norv
34	46	46.9	641	1	XKR6_HUMAN	Q5gh73 homo sapien
35	46	46.9	807	1	SYL_CHLTE	Q8kyb2 chlorobium
36	46	46.9	836	2	Q2Y8V4_NITMU	Q2y8v4 nitrospiral
37	46	46.9	859	2	Q3XW00_MAGNETO	Q3xw00 magnetococc
38	46	46.9	863	2	Q2S415_9SPHI	Q2s415 salinibacte
39	46	46.9	2484	2	Q5CPZ7_CRYPV	Q5cpz7 cryptospori
40	45	45.9	178	2	Q9RYR0_DEIRA	Q9ryr0 deinococcus
41	45	45.9	219	2	Q6LIT5_PICTO	Q6lit5 picophilus
42	45	45.9	276	2	Q4BS81_BURVI	Q4bs81 burkholderi
43	45	45.9	278	2	Q7VU93_BORPE	Q7vu93 bordetella
44	45	45.9	278	2	Q7W7P3_BORPA	Q7w7p3 bordetella
45	45	45.9	278	2	Q7WL31_BORBR	Q7wl31 bordetella

ALIGNMENTS

RESULT 1
ID Q3APY5_CHLCH PRELIMINARY; PRT; 805 AA.
AC Q3APY5_ CHLCH
DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, sequence version 1.
DE Leucyl-tRNA synthetase class Ia (EC 6.1.1.4).
GN OrderedLocusNames=Cag_1688;
OS Chlorobium chlorochromatii (strain Cad3).
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium/Pelodictyon group; Chlorobium.
OX NCBI_TaxID=340177;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Israeli S., Pittluck S., Bryant D., Schmutz J., Larimer F.,
RA Land M., Kyripides N., Ivanova N., Richardson P.,
RA "Complete sequence of Chlorobium chlorochromatii Cad3."
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC EMBL; CP000108; ABB28940.1; -; Genomic_DNA.
DR GO; GO:0005324; P:ATP binding; IEA.
DR GO; GO:0004823; P:leucine-tRNA ligase activity; IEA.
DR GO; GO:0016874; P:ligase activity; IEA.
DR GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
KW Aminoacyl-tRNA synthetase; Complete proteome; Ligase.
SQ SEQUENCE 805 AA; 92007 MW; AOC78B83732AF54C CRC64;

Query Match 59.2%; Score 58; DB 2; Length 805;
Best Local Similarity 69.2%; Pred No. 3.2; Indels 0; Gaps 0;
Matches 9; Conservative 2; Mismatches 2;

Qy 1 GIRRFLGSIWRFI 13
||| :||| :||| :
Db 622 GISRFLCKWRFV 634

RESULT 2
ID Q25271_LEPDE PRELIMINARY; PRT; 670 AA.
AC Q25271_ LEPDE
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DE Diapause protein 1 (Fragment).
GN Name=Dp19;
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;

GO: GO:0015031; P:protein transport; IEA.
GO: GO:0006508; P:proteolysis; IEA.
InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR011527; ABC_TM_1.
DR InterPro: IPR001140; ABC_TM_transpt.
DR InterPro: IPR003439; ABC_transp_like.
DR InterPro: IPR005074; Peptidase_C39.
DR InterPro: IPR010132; Type_I_sec_HlyB.
DR PANTHER: PTHR19242:SF74; Type_I_sec_HlyB; 1.
DR Pfam: PF00664; ABC_membrane; 1.
DR Pfam: PF00005; ABC_tran; 1.
DR Pfam: PF03412; Peptidase_C39; 1.
DR ProDom: PD000006; ABC_transporter; 1.
DR SMART: SM00382; AAA; 1.
DR TIGRfams: TIGR01846; type_I_sec_HlyB; 1.
DR PROSITE: PS50929; ABC_TMIF; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE: PS50893; ABC_TRANSPORTER_2; 1.
DR PROSITE: PS50990; PEPTIDASE_C39; 1.
SQ SEQUENCE 735 AA; 80717 MW; 0216259241F3630C CRC64;

Query Match 53.1%; Score 52; DB 2; Length 735;
Best Local Similarity 62.5%; Pred.No. 26;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRRFGLSIWRFIRAF 16
 | | | | | : | | | : | | |
DB 161 GFRWFPLAIWRYRRAF 176

RESULT 4

Q44QD1_CHLLI
ID Q44QD1_CHLLI PRELIMINARY; PRT; 805 AA.
AC Q44QD1
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 21-FEB-2006, entry version 9.
DE Leucyl-tRNA synthetase bacterial/mitochondrial, class Ia.
OS ORFNames=ClimDRAFT_1980;
GN Chlorobium limicola DSM 245.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium/felodictyon group; Chlorobium.
NCBI_TaxID=290315;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 245;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.,
RA "Sequencing of the draft genome and assembly of Chlorobium limicola
RT DSM 245.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 245;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.,
RA "Annotation of the draft genome assembly of Chlorobium limicola DSM
RT 245.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License

CC EMBL: AAJ01000009; EAM43320.1; -; Genomic_DNA.
DR GO: GO:0005524; P:ATP binding; IEA.
DR GO: GO:0004823; P:leucine-tRNA ligase activity; IEA.
DR GO: GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
DR InterPro: IPR002302; Leu_tRNA_synth_Ia.
DR Pfam: PF001133; tRNA-synt_1; 1.

```

DR PRINTS; PRO0985; TRNASYNTHLEU.
KW Aminoacyl-tRNA synthetase_bact; 1.
SQ SEQUENCE 805 AA; 91997 MW; D4F3FE28F9E92DF3 CRC64;

Query Match 53.1%; Score 52; DB 2; Length 805;
Best Local Similarity 61.5%; Pred. No. 29;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GIRRFGLSIWRFFI 13
Db 622 GISRFLGKVRRLV 634

RESULT 5
O43K01_9CHLB PRELIMINARY; PRT; 816 AA.
ID O43K01_9CHLB
AC O43K01
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, entry version 9.
DE Leucyl-tRNA synthetase bacterial/mitochondrial, class Ia.
GN ORFNames=cpa266DRAFT_2546;
OS Chlorobium phaeobacteroides DSM 266.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium/Pelodictyon group; Chlorobium.
OX NCBI_TaxID=290317;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 266;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.,
RA "Sequencing of the draft genome and assembly of Chlorobium
RT phaeobacteroides DSM 266.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 266;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Chlorobium
RT phaeobacteroides DSM 266.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; AAI01000002; EMB35935.1; Genomic_DNA.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
DR GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
DR InterPro; IPR002302; Leu_tRNA_synth_1a.
DR Pfam; PF00133; tRNA-synth_1; 1.
DR PRINTS; PRO0985; TRNASYNTHLEU.
DR TIGRFAMs; TIGR00396; leus_bact; 1.
KW Aminoacyl-tRNA synthetase.
SQ SEQUENCE 816 AA; 93335 MW; 6770B1DAC50560F1 CRC64;

Query Match 53.1%; Score 52; DB 2; Length 816;
Best Local Similarity 61.5%; Pred. No. 29;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GIRRFGLSIWRFFI 13
Db 622 GISRFLGKVRRLV 634

RESULT 6
Q39L57_BURS3 PRELIMINARY; PRT; 407 AA.
ID Q39L57;
AC Q39L57;
DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, entry version 4.
DE Hypothetical protein.
GN OrderedLocuNames=Bcep18194_A3207;
OS Burkholderia sp. (strain 383) (Burkholderia cepacia (strain ATCC 17760
/ NCIB 9086 / R18194)).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=269483;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Chain P., Malfatti S., Shin M.,
RA Vergez L., Schmutz J., Larimer F., Land M., Kyrpides N., Lykidis A.,
RA Richardson P.;
RA "Complete sequence of chromosome 1 of Burkholderia sp. 383.";
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; CP000151; AB06809.1; Genomic_DNA.
DR Complete proteome; Hypothetical protein.
KW SEQUENCE 407 AA; 45483 MW; 957829B27BCABFC1 CRC64;
SQ SEQUENCE 407 AA; 45483 MW; 957829B27BCABFC1 CRC64;

Query Match 52.0%; Score 51; DB 2; Length 407;
Best Local Similarity 47.1%; Pred. No. 20;
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GIRRFGLSIWRFFIRAFY 17
Db 327 GIRQMLGHVQWTRSSY 343

RESULT 7
O456F4_9BURK PRELIMINARY; PRT; 408 AA.
ID O456F4_9BURK
AC O456F4;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 2.
DE Hypothetical protein.
GN ORFNames=BcendRAFT_3751;
OS Burkholderia cenocepacia AU 1054.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX NCBI_TaxID=331271;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AU 1054;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RA "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT AU 1054.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AU 1054;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT AU 1054.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms

```


Name=	XK87; Synonyms=C20orf159, XKG7;
GN	Homo sapiens (Human).
OS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OCC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC	Homo.
NB	NCBI_TaxID=9606;
RN	[1]_TaxID=9606;
NN	
RP	NUCLEOTIDE SEQUENCE [MRNA].
RA	Huang C.-H., Chen Y.;
RT	"A superfamily of XK-related genes (XKG) widely expressed in vertebrates and invertebrates.";
RJL	Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
RRL	[2]
RRR	SEQUENCE [LARGE SCALE GENOMIC DNA].
RRP	MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RRX	Jeloukas P., Matthews L.H., Ashurst J.L., Burton J.J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L., Bailey J., Barlow K.F., Blake K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blake S.E., Bridgman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark R., Clark L.N., Clark S.V., Clee C.M., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhami F.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Graham D.V., Griffiths C., Griffiths M.N.D., Gilliland R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle B., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Leivaeslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.I., McConachie L.J., McLay K., McMurray A.A., Milne S.A., Mastry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Symcote N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaubin M., Wall M., Wallis J.W., Williams S.A., Whitehead S.L., Whittaker P., Willet D.L., Williams L., Williams S.A., Wingling L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J.;
RNA	The DNA sequence and comparative analysis of human chromosome 20.;"
RTL	Nature 414:865-871(2001). Membrane; multi-pass membrane protein
RTC	(Potential).
CCC	-! SIMILARITY: Belongs to the XK family.
CCC	-! CAUTION: Ref.2 sequence differs from that shown due to erroneous gene model prediction.
CCCC	-----
CCCCC	Coprighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
CCCCCC	EMBL; AY534245; AAAT07094.1; -; mRNA.
CCCCC	EMBL; ALU031658; CAB86102.1; ALT SEQ: Genomic_DNA.
DD	Ensembl; ENSGEN0000101321; Homo sapiens.
DR	HGNC; HGNC:23062; XK87.
DW	Membrane; Transmembrane.
KW	CHAIN 1 579
FT	XK-related protein 7.
FFT	/FTId=PRO_0000190788.
FTT	Potential.
FTT	TRANSMEM 59 79
FTF	Potential.
FF	TRANSMEM 89 109
FFF	Potential.
FFFF	TRANSMEM 260 280
TTTT	Potential.
TTF	TRANSMEM 314 334
TTF	Potential.
TTT	TRANSMEM 355 375
TTT	Potential.
TTT	TRANSMEM 384 404
TTT	Potential.
TTT	TRANSMEM 415 435
SQ	SEQUENCE 579 AA; 63826 MW; D8D0FF64B9EDED53D CRC64;
Query Match 51.0%; Score 50; DB 1; Length 579;	
Best Local Similarity 58.3%; Pred.No. 42;	
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;	
: :	
6 LGSIWRFPAPY 17 QY	


```
Db      190 LGQVRYLRALY 201

RESULT 10
ID      XKR7 PANTR      STANDARD;      PRT;      579 AA.
AC      Q49LS1;
DT      11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT      13-SEP-2005, sequence version 1.
DT      07-FEB-2006, entry version 6.
DE      XK-related protein 7.
GN      Name=XKR7; Synonyms=XRG7;
OS      Pan troglodytes (Chimpanzee).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC      Pan.
OX      NCBI_TaxID=9598;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [MRNA].
RA      Huang C.-H., Chen Y.;
RT      "A superfamily of XK-related genes (XRG) widely expressed in
RL      vertebrates and invertebrates."
RL      Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC      -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC      (Potential).
CC      -!- SIMILARITY: Belongs to the XK family.
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
CC      EMBL; AY702910; AAV83783.1; -; mRNA.
KW      Membrane; Transmembrane.
FT      CHAIN          1      579
FT      TRANSMEM      59      79
FT      TRANSMEM      89      109
FT      TRANSMEM      260     280
FT      TRANSMEM      314     334
FT      TRANSMEM      355     375
FT      TRANSMEM      384     404
FT      TRANSMEM      415     435
FT      TRANSMEM      415     435
SQ      SEQUENCE      579 AA; 63593 MW; 6DFE1191093E85D4 CRC64;

Query Match          51.0%; Score 50; DB 1; Length 579;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      6 LGSWRFIRAFY 17
ID      XKR7 MOUSE      STANDARD;      PRT;      580 AA.
AC      Q5GH64;
DT      11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT      01-MAR-2005, sequence version 1.
DT      07-FEB-2006, entry version 10.
DE      XK-related protein 7.
GN      Name=Xkr7; Synonyms=Xrg7;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Murioidea; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [MRNA].
RA      Huang C.-H., Chen Y.;
RT      "A superfamily of XK-related genes (XRG) widely expressed in
RL      vertebrates and invertebrates."
RL      Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC      -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC      (Potential).
CC      -!- SIMILARITY: Belongs to the XK family.
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
CC      EMBL; AY534261; AAT07110.1; -; mRNA.
KW      Membrane; Transmembrane.
FT      CHAIN          1      580
FT      TRANSMEM      59      79
FT      TRANSMEM      89      109
FT      TRANSMEM      260     280
FT      TRANSMEM      303     323
FT      TRANSMEM      326     346
FT      TRANSMEM      355     375
FT      TRANSMEM      384     404
FT      TRANSMEM      415     435
FT      TRANSMEM      415     435
SQ      SEQUENCE      580 AA; 64302 MW; F3291FABF4C5A826 CRC64;

Query Match          51.0%; Score 50; DB 1; Length 580;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      6 LGSWRFIRAFY 17
ID      XKR7 RAT          STANDARD;      PRT;      580 AA.
AC      Q5GH56;
DT      11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT      01-MAR-2005, sequence version 1.
DT      07-FEB-2006, entry version 8.
DE      XK-related protein 7.
GN      Name=Xkr7; Synonyms=Xrg7;
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muroidae; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [MRNA].
RA      Huang C.-H., Chen Y.;
RT      "A superfamily of XK-related genes (XRG) widely expressed in
RL      vertebrates and invertebrates."
RL      Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC      -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC      (Potential).
CC      -!- SIMILARITY: Belongs to the XK family.
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
CC      EMBL; AY534261; AAT07110.1; -; mRNA.
KW      Membrane; Transmembrane.
FT      CHAIN          1      580
FT      TRANSMEM      59      79
FT      TRANSMEM      89      109
FT      TRANSMEM      260     280
FT      TRANSMEM      303     323
FT      TRANSMEM      326     346
FT      TRANSMEM      355     375
FT      TRANSMEM      384     404
FT      TRANSMEM      415     435
FT      TRANSMEM      415     435
SQ      SEQUENCE      580 AA; 64338 MW; 8F4907F391B4F5BE CRC64;
```

```
CC      -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC      (Potential).
CC      -!- SIMILARITY: Belongs to the XK family.
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
CC      EMBL; AY534253; AAT07102.1; -; mRNA.
DR      Ensembl; ENSMUSG00000042631; Mus musculus.
DR      MGI; MGI:3526711; Xkr7.
KW      Membrane; Transmembrane.
FT      CHAIN          1      580
FT      TRANSMEM      59      79
FT      TRANSMEM      89      109
FT      TRANSMEM      260     280
FT      TRANSMEM      303     323
FT      TRANSMEM      326     346
FT      TRANSMEM      355     375
FT      TRANSMEM      384     404
FT      TRANSMEM      415     435
FT      TRANSMEM      415     435
SQ      SEQUENCE      580 AA; 64302 MW; F3291FABF4C5A826 CRC64;

Query Match          51.0%; Score 50; DB 1; Length 580;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      6 LGSWRFIRAFY 17
ID      XKR7 RAT          STANDARD;      PRT;      580 AA.
AC      Q5GH56;
DT      11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT      01-MAR-2005, sequence version 1.
DT      07-FEB-2006, entry version 8.
DE      XK-related protein 7.
GN      Name=Xkr7; Synonyms=Xrg7;
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muroidae; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [MRNA].
RA      Huang C.-H., Chen Y.;
RT      "A superfamily of XK-related genes (XRG) widely expressed in
RL      vertebrates and invertebrates."
RL      Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC      -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC      (Potential).
CC      -!- SIMILARITY: Belongs to the XK family.
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
CC      EMBL; AY534261; AAT07110.1; -; mRNA.
KW      Membrane; Transmembrane.
FT      CHAIN          1      580
FT      TRANSMEM      59      79
FT      TRANSMEM      89      109
FT      TRANSMEM      260     280
FT      TRANSMEM      303     323
FT      TRANSMEM      326     346
FT      TRANSMEM      355     375
FT      TRANSMEM      384     404
FT      TRANSMEM      415     435
FT      TRANSMEM      415     435
SQ      SEQUENCE      580 AA; 64338 MW; 8F4907F391B4F5BE CRC64;
```



```
RX MEDLINE=22417727; PubMed=12529541; DOI=10.1104/pp.012963;
RA Davidson S.E., Elliott R.C., Helliwell C.A., Poole A.T., Reid J.B.;
RT "The pea gene NA encodes ent-kaurenoic acid oxidase.";
RL Plant Physiol. 131:335-344(2003).
CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum (By
CC similarity).
CC -!- SIMILARITY: Belongs to the cytochrome P450 family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AF537321; AA023063.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR02401; EP450I.
DR PANTHER; PTHR19383; Cytochrome_P450; 1.
DR Pfam; PF00067; P450; 2.
DR PRINTS; PR00463; EP450I.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
KW Endoplasmic reticulum; Heme; Iron; Membrane; Metal-binding;
KW Monooxygenase; Oxidoreductase.
SQ SEQUENCE 488 AA; 56478 MW; 503453CB6E43C830 CRC64;

Query Match 50.0%; Score 49; DB 2; Length 488;
Best Local Similarity 58.3%; Pred. No. 50;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 5.FLGSINRPIRAF 16
|:|:| |:|
Db 54.FIGNWSFLRAF 65

Search completed: May 19, 2006, 14:38:12
Job time : 124.429 secs
```

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:38:42 ; Search time 24.8571 Seconds
(without alignments)
63.384 Million cell updates/sec

Title: US-10-712-447-13

Perfect score: 98

Sequence: 1 GRRFLGSIWRFIRAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:**
- 1: /EMC Celerra_SIDS3/ptodata/2/iaa/5 COMB.pdp.*
 - 2: /EMC Celerra_SIDS3/ptodata/2/iaa/6 COMB.pdp.*
 - 3: /EMC Celerra_SIDS3/ptodata/2/iaa/7 COMB.pdp.*
 - 4: /EMC Celerra_SIDS3/ptodata/2/iaa/H COMB.pdp.*
 - 5: /EMC Celerra_SIDS3/ptodata/2/iaa/PCTUS COMB.pdp.*
 - 6: /EMC Celerra_SIDS3/ptodata/2/iaa/RE COMB.pdp.*
 - 7: /EMC Celerra_SIDS3/ptodata/2/iaa/backfilese1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	79.6	18	2	US-08-940-095-242
2	78	79.6	18	2	US-08-940-093-242
3	78	79.6	18	2	US-08-940-096-242
4	78	79.6	18	2	US-09-465-719-242
5	78	79.6	18	2	US-09-453-605-242
6	78	79.6	18	2	US-09-453-838-242
7	78	79.6	18	2	US-08-940-136-242
8	78	79.6	18	2	US-09-453-841-242
9	78	79.6	18	2	US-09-453-833-242
10	78	79.6	18	2	US-09-453-826-242
11	78	79.6	18	2	US-09-453-840-242
12	78	79.6	18	2	US-09-865-989-242
13	78	79.6	18	2	US-09-453-834-242
14	78	79.6	18	2	US-10-283-599-242
15	78	79.6	18	2	US-09-465-718-242
16	51	52.0	76	2	US-09-205-258-892
17	51	52.0	76	2	US-10-004-860-892
18	47.5	48.5	253	2	US-09-586-106D-49
19	47.5	48.5	253	2	US-10-799-870-49
20	45.5	46.4	254	2	US-09-586-106D-45
21	45.5	46.4	254	2	US-10-799-870-45
22	45	45.9	22	1	US-08-338-882-40
23	45	45.9	22	1	US-08-338-882-41
24	45	45.9	539	2	US-09-710-279-340
25	45	45.9	835	2	US-09-134-001C-5105
26	45	45.9	877	2	US-09-328-352-8162

27	44	44.9	22	1	US-08-132-767-50	Sequence 50, Appl
28	44	44.9	589	1	US-08-756-317-5	Sequence 5, Appl1
29	44	44.9	1052	2	US-09-134-000C-6620	Sequence 6620, Ap
30	43	43.9	23	2	US-10-360-101-83	Sequence 83, Appl
31	43	43.9	413	3	US-09-609-146-27	Sequence 27, Appl
32	43	43.9	439	3	US-09-609-146-29	Sequence 29, Appl
33	43	43.9	683	2	US-09-502-540-15932	Sequence 15932, A
34	43	43.9	702	2	US-10-094-749-2262	Sequence 2462, Ap
35	43	43.9	812	2	US-09-538-092-643	Sequence 643, Appl
36	42	42.9	14	1	US-08-480-190-3	Sequence 3, Appl1
37	42	42.9	14	1	US-08-488-379-3	Sequence 3, Appl1
38	42	42.9	14	2	US-08-475-399A-3	Sequence 3, Appl1
39	42	42.9	14	5	PCT-US93-07545-3	Sequence 3, Appl1
40	42	42.9	15	1	US-08-480-190-2	Sequence 2, Appl1
41	42	42.9	15	1	US-08-488-379-2	Sequence 2, Appl1
42	42	42.9	15	2	US-08-475-399A-2	Sequence 2, Appl1
43	42	42.9	15	2	US-08-077-255A-2	Sequence 2, Appl1
44	42	42.9	15	5	PCT-US93-07545-2	Sequence 2, Appl1
45	42	42.9	15	5	PCT-US93-07545-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-940-095-242
; Sequence 242, Application US/08940095
; Patent No. 6004925
; GENERAL INFORMATION:
; APPLICANT: Daseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Butner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,095
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6004925e
US-08-940-095-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFVG 18
||:|||||:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 2

US-08-940-093-242
; Sequence 242, Application US/08940093
; Patent No. 6037323
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,093
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6037323e
; US-08-940-093-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFVG 18
||:|||||:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 3

US-08-940-096-242
; Sequence 242, Application US/08940096
; Patent No. 6046166
; GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,096
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6046166e
; US-08-940-096-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFVG 18
||:|||||:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 4

US-09-465-719-242
; Sequence 242, Application US/09465719
; Patent No. 6265377
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/465,719
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,093
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6265377e
; US-09-465-719-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFVG 18
||:|||||:|:|
Db 1 GIKKFLGSIWKFIFAFVG 18

RESULT 5
US-09-453-605-242
; Sequence 242, Application US/09453605
; Patent No. 6329341
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,605
; FILING DATE: 26-NO. 6329341-1999
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
```

```
;
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6329341e
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:
; US-09-453-605-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFVG 18
||:|||||:|:|
Db 1 GIKKFLGSIWKFIFAFVG 18

RESULT 6
US-09-453-838-242
; Sequence 242, Application US/09453838
; Patent No. 6376464
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,838
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6376464e
```

US-09-453-838-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRKFLGSIWRFIRAFVG 18
|:::|||||:|:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 7

US-08-940-136-242

; Sequence 242, Application US/08940136
; Patent No. 6518412

; GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis

; APPLICANT: Sekul, Renate

; APPLICANT: Buttner, Klaus

; APPLICANT: Cornut, Isabelle

; APPLICANT: Dufourcq, Jean

; TITLE OF INVENTION: GENE THERAPY APPROACHES TO

; TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR

; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.

; NUMBER OF SEQUENCES: 274

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036-2811

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/940,136

; FILING DATE: 29-SEP-1997

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 009196-0007-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-493-4935

; TELEFAX: 650-493-5556

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 242:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: No. 6518412e

US-08-940-136-242

Query Match

79.6%; Score 78; DB 2; Length 18;

Best Local Similarity 72.2%; Pred. No. 1.1e-05;

Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRKFLGSIWRFIRAFVG 18
|:::|||||:|:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 8

US-09-453-841-242

; Sequence 242, Application US/09453841

; Patent No. 6573239

; GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis

; APPLICANT: Sekul, Renate

; APPLICANT: Buttner, Klaus

; APPLICANT: Cornut, Isabelle

; APPLICANT: Metz, Gunther

; APPLICANT: Dufourcq, Jean

; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

; NUMBER OF SEQUENCES: 258

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036-2811

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/453,841

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/940,095

; FILING DATE: 29-SEP-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 009196-0004-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-493-4935

; TELEFAX: 650-493-5556

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 242:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: No. 6573239e

US-09-453-841-242

Query Match 79.6%; Score 78; DB 2; Length 18;

Best Local Similarity 72.2%; Pred. No. 1.1e-05;

Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRKFLGSIWRFIRAFVG 18
|:::|||||:|:|:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 9

US-09-453-833-242

; Sequence 242, Application US/09453833

; Patent No. 6602854

; GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis

; APPLICANT: Sekul, Renate

; APPLICANT: Buttner, Klaus

; APPLICANT: Cornut, Isabelle

; APPLICANT: Metz, Gunther

; APPLICANT: Dufourcq, Jean

; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

; NUMBER OF SEQUENCES: 258

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,833
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6602854e
US-09-453-833-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFYG 18
Db 1 GIKKFLGSIWKFIRAFVG 18

RESULT 10
US-09-453-826-242
Sequence 242, Application US/09453826
Patent No. 6630450
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,826
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6630450e
US-09-453-826-242

Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFLGSIWRFIRAFYG 18
Db 1 GIKKFLGSIWKFIRAFVG 18

RESULT 11
US-09-453-840-242
Sequence 242, Application US/09453840
Patent No. 6716816
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,840
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids

```
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6716816e
US-09-453-840-242
Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFVG 18
|:::|||||:|:|
Db 1 GIKKFLGSIWKFIRAFVG 18

RESULT 12
US-09-865-989-242
; Sequence 242, Application US/09865989
; Patent No. 6734169
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION NUMBER: US/09/865,989
; FILING DATE: 25-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/465,719
; FILING DATE: 17-DEC-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6734169e
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-865-989-242
Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFVG 18
|:::|||||:|:|
Db 1 GIKKFLGSIWKFIRAFVG 18

TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION NUMBER: US/09/865,989
FILING DATE: 25-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/465,719
FILING DATE: 17-DEC-1999
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6734169e
SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-865-989-242
Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFVG 18
|:::|||||:|:|
Db 1 GIKKFLGSIWKFIRAFVG 18
```

```
RESULT 13
US-09-453-834-242
; Sequence 242, Application US/09453834
; Patent No. 6753313
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,834
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 08/940,095
; APPLICATION NUMBER:
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6753313e
; US-09-453-834-242
Query Match 79.6%; Score 78; DB 2; Length 18;
Best Local Similarity 72.2%; Pred. No. 1.1e-05;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFLGSIWRFIRAFVG 18
|:::|||||:|:|
Db 1 GIKKFLGSIWKFIRAFVG 18

RESULT 14
US-10-283-599-242
; Sequence 242, Application US/10283599
; Patent No. 6844327
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
```

;; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.

;; NUMBER OF SEQUENCES: 274

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Pennie & Edmonds LLP

;; STREET: 1155 Avenue of the Americas

;; CITY: New York

;; STATE: NY

;; COUNTRY: USA

;; ZIP: 10036-2811

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: DOS

;; SOFTWARE: FastSEQ Version 2.0

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/10/283,599

;; FILING DATE: 29-OCT-2002

;; CLASSIFICATION:

;; APPLICATION NUMBER: 08/940,136

;; FILING DATE: 29-SEP-1997

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Coruzzi, Laura A

;; REGISTRATION NUMBER: 30,742

;; REFERENCE/DOCKET NUMBER: 009196-0007-999

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 650-493-4935

;; TELEFAX: 650-493-5556

;; TELEX: 66141 PENNIE

;; INFORMATION FOR SEQ ID NO: 242:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 18 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: No. 6844327e

;; US-10-283-599-242

Query Match 79.6%; Score 78; DB 2; Length 18;

Best Local Similarity 72.2%; Pred. No. 1.1e-05;

Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRPIAFYVG 18

Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 15

US-09-465-718-242

;; Sequence 242, Application US/09465718

;; Patent No. 6900177

;; GENERAL INFORMATION:

;; APPLICANT: Dasseux, Jean-Louis

;; APPLICANT: Sekul, Renate

;; APPLICANT: Buttner, Klaus

;; APPLICANT: Cornut, Isabelle

;; APPLICANT: Metz, Gunther

;; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

;; NUMBER OF SEQUENCES: 258

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Pennie & Edmonds LLP

;; STREET: 1155 Avenue of the Americas

;; CITY: New York

;; STATE: NY

;; COUNTRY: USA

;; ZIP: 10036-2811

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: DOS

;; SOFTWARE: FastSEQ Version 2.0

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/465,718

;; FILING DATE: 17-Dec-1999

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US/08/940,096

;; FILING DATE: 29-SEP-1997

;; APPLICATION NUMBER:

;; FILING DATE:

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Coruzzi, Laura A

;; REGISTRATION NUMBER: 30,742

;; REFERENCE/DOCKET NUMBER: 009196-0005-999

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 650-493-4935

;; TELEFAX: 650-493-5556

;; TELEX: 66141 PENNIE

;; INFORMATION FOR SEQ ID NO: 242:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 18 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: No. 6900177e

;; US-09-465-718-242

Query Match

Best Local Similarity 72.2%; Score 78; DB 2; Length 18;

Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRPIAFYVG 18

Db 1 GIKKFLGSIWKFIKAFVG 18

Search completed: May 19, 2006, 14:42:54

Job time : 25.8571 secs

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 15:18:19 ; Search time 81.2857 Seconds
(without alignments)
102.575 Million cell updates/sec

Title: US-10-712-447-13

Perfect score: 98

Sequence: 1 GIRFLGSIWRFIRAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	18	4	US-10-712-447-2
2	98	100.0	18	4	US-10-712-447-5
3	98	100.0	18	4	US-10-712-447-8
4	98	100.0	18	4	US-10-712-447-10
5	98	100.0	18	4	US-10-712-447-13
6	95	96.9	18	4	US-10-712-447-91
7	94	95.9	18	4	US-10-712-447-115
8	94	95.9	18	4	US-10-712-447-116
9	94	95.9	18	4	US-10-712-447-117
10	94	95.9	18	4	US-10-712-447-129
11	94	95.9	18	4	US-10-712-447-131
12	92	93.9	18	4	US-10-712-447-21
13	92	93.9	18	4	US-10-712-447-53
14	92	93.9	18	4	US-10-712-447-74
15	90	91.8	18	4	US-10-712-447-4
16	90	91.8	18	4	US-10-712-447-127
17	89	90.8	18	4	US-10-712-447-99
18	88	89.8	18	4	US-10-712-447-18
19	88	89.8	18	4	US-10-712-447-112
20	88	89.8	18	4	US-10-712-447-113
21	88	89.8	18	4	US-10-712-447-114
22	87	88.8	18	4	US-10-712-447-17
23	86	87.8	18	4	US-10-712-447-61
24	86	87.8	18	4	US-10-712-447-82
25	85	86.7	18	4	US-10-712-447-16
26	85	86.7	18	4	US-10-712-447-96
27	85	86.7	18	4	US-10-712-447-121

28	84	85.7	18	4	US-10-712-447-22	Sequence 22, Appl
29	84	85.7	18	4	US-10-712-447-78	Sequence 78, Appl
30	84	85.7	18	4	US-10-712-447-95	Sequence 95, Appl
31	84	85.7	18	4	US-10-712-447-120	Sequence 120, Appl
32	82	83.7	18	4	US-10-712-447-19	Sequence 19, Appl
33	82	83.7	18	4	US-10-712-447-56	Sequence 56, Appl
34	82	83.7	18	4	US-10-712-447-58	Sequence 58, Appl
35	82	83.7	18	4	US-10-712-447-77	Sequence 77, Appl
36	82	83.7	18	4	US-10-712-447-79	Sequence 80, Appl
37	82	83.7	18	4	US-10-712-447-80	Sequence 94, Appl
38	82	83.7	18	4	US-10-712-447-94	Sequence 99, Appl
39	81	82.7	18	4	US-10-712-447-57	Sequence 57, Appl
40	81	82.7	18	4	US-10-712-447-100	Sequence 100, Appl
41	80	81.6	18	4	US-10-712-447-41	Sequence 41, Appl
42	79	80.6	18	4	US-10-712-447-97	Sequence 97, Appl
43	78	79.6	18	3	US-09-865-989-242	Sequence 242, Appl
44	78	79.6	18	3	US-09-865-989-242	Sequence 242, Appl
45	78	79.6	18	4	US-10-099-574A-242	Sequence 242, Appl

ALIGNMENTS

RESULT 1
US-10-712-447-2
; Sequence 2, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; OTHER INFORMATION: c-term amidated
US-10-712-447-2

Query Match 100.0%; Score 98; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 9.8e-08; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

Qy 1 GIRFLGSIWRFIRAFYG 18

Db 1 GIRFLGSIWRFIRAFYG 18

RESULT 2

US-10-712-447-5
; Sequence 5, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13

```
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-5

Query Match          100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
Db 1 GRRFLGSIWRFIRAFYG 18

RESULT 3
US-10-712-447-8
; Sequence 8, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-8

Query Match          100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
Db 1 GRRFLGSIWRFIRAFYG 18

RESULT 4
US-10-712-447-10
; Sequence 10, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-10

Query Match          100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
Db 1 GRRFLGSIWRFIRAFYG 18

RESULT 5
US-10-712-447-13
; Sequence 13, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-13

Query Match          100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.8e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFLGSIWRFIRAFYG 18
Db 1 GRRFLGSIWRFIRAFYG 18

RESULT 6
US-10-712-447-91
; Sequence 91, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; PRIOR FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 91
; LENGTH: 18
```



```
; OTHER INFORMATION: peptide
US-10-712-447-74
Query Match          93.9%; Score 92; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 7.9e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18
   |||..|||..|||..|||
Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 15
US-10-712-447-4
; Sequence 4, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712.447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-4
Query Match          91.8%; Score 90; DB 4; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.6e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFLGSIWRFIRAFYG 18
   |||..|||..|||..|||
Db 1 GIRRFLGSIWRFIRAFYG 18

Search completed: May 19, 2006, 15:27:56
Job time : 81.2857 secs
```

This Page Blank (uspto)

; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 12848, 13875,
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
; FILE REFERENCE: MPI2001-288P1RCP10NMIM
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-11-242-505A-18

Query Match 37.8%; Score 37; DB 7; Length 403;
Best Local Similarity 55.6%; Pred. No. 16;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 IRRFLGSIW 10
: || ||| :
Db 155 VRRVLGAV 163

RESULT 3
US-09-949-925-142
; Sequence 142, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 142
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (60)
; OTHER INFORMATION: Xaa equals stop translation
US-09-949-925-142

Query Match 37.2%; Score 36.5; DB 1; Length 60;
Best Local Similarity 57.1%; Pred. No. 2.2;
Matches 8; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
QY 5 FLGSIWRFIRAFYG 18
: || : ||| :
Db 31 FLILVWIFV-AFYG 43

RESULT 4
US-09-949-925-111
; Sequence 111, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (74)
; OTHER INFORMATION: Xaa equals stop translation
US-09-949-925-111

Query Match 36.7%; Score 36; DB 1; Length 74;
Best Local Similarity 54.5%; Pred. No. 3.3;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IRRFLGSIWRF 12
: || ||| :
Db 59 LREVSGKIWRF 69

RESULT 5
US-11-302-678-5
; Sequence 5, Application US/11302678
; Publication No. US20060088881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318,
; FILE REFERENCE: MPI02-012P1RNM_OMNI

;; CURRENT APPLICATION NUMBER: US/11/302,678
;; CURRENT FILING DATE: 2005-12-14
;; PRIOR APPLICATION NUMBER: US/10/345,680
;; PRIOR FILING DATE: 2003-01-16
;; PRIOR APPLICATION NUMBER: US 60/349,511
;; PRIOR FILING DATE: 2002-01-18
;; PRIOR APPLICATION NUMBER: US 60/360,500
;; PRIOR FILING DATE: 2002-02-28
;; PRIOR APPLICATION NUMBER: US 60/365,041
;; PRIOR FILING DATE: 2002-03-15
;; PRIOR APPLICATION NUMBER: US 60/374,063
;; PRIOR FILING DATE: 2002-04-19
;; PRIOR APPLICATION NUMBER: US 60/403,468
;; PRIOR FILING DATE: 2002-08-14
;; PRIOR APPLICATION NUMBER: US 60/414,262
;; PRIOR FILING DATE: 2002-09-27
;; PRIOR APPLICATION NUMBER: US 60/419,986
;; PRIOR FILING DATE: 2002-10-21
;; PRIOR APPLICATION NUMBER: US 60/423,809
;; PRIOR FILING DATE: 2002-11-05
;; PRIOR APPLICATION NUMBER: US 60/429,797
;; PRIOR FILING DATE: 2002-11-26
;; NUMBER OF SEQ ID NOS: 66
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 5
;; LENGTH: 599
;; TYPE: PRT
;; ORGANISM: Homo Sapiens
US-11-302-678-5

Query Match 36.7%; Score 36; DB 7; Length 599;
Best Local Similarity 71.4%; Pred. No. 38;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 LGSWRF 12
Db 64 LGSWRF 70

RESULT 6
US-11-242-505A-48
;; Sequence 48, Application US/11242505A
;; Publication No. US2006009656A1
;; GENERAL INFORMATION:
;; APPLICANT: Carroll, Joseph M.
;; APPLICANT: Healy, Aileen
;; TITLE OF INVENTION: Methods and Compositions for Treating
;; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
;; FILE REFERENCE: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
;; CURRENT APPLICATION NUMBER: US/11/242,505A
;; CURRENT FILING DATE: 2005-10-03
;; PRIOR APPLICATION NUMBER: US 10/290,078
;; PRIOR FILING DATE: 2002-11-07
;; PRIOR APPLICATION NUMBER: US 60/347,949
;; PRIOR FILING DATE: 2001-11-07
;; PRIOR APPLICATION NUMBER: US 10/320,351
;; PRIOR FILING DATE: 2002-12-16
;; PRIOR APPLICATION NUMBER: 60/341,606
;; PRIOR FILING DATE: 2001-12-17
;; NUMBER OF SEQ ID NOS: 48
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 48
;; LENGTH: 313
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-242-505A-48

Query Match 34.7%; Score 34; DB 7; Length 313;
Best Local Similarity 50.0%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 6 LGSWRF 17

Db 195 LEEAFLDAFY 206

RESULT 7
US-10-511-937-2540
;; Sequence 2540, Application US/10511937
;; Publication No. US2006008836A1
;; GENERAL INFORMATION:
;; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
;; APPLICANT: Wohlseuth, Jay
;; APPLICANT: Fry, Kirk, Robert
;; APPLICANT: Woodward, Robert
;; APPLICANT: Ly, Ngoc
;; APPLICANT: Prentice, James
;; APPLICANT: Morris, MacDonald
;; APPLICANT: Rosenberg, Steven
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
;; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
;; FILE REFERENCE: 506612000104
;; CURRENT APPLICATION NUMBER: US/10/511,937
;; CURRENT FILING DATE: 2004-10-19
;; PRIOR APPLICATION NUMBER: PCT/US2003/012946
;; PRIOR FILING DATE: 2003-04-24
;; PRIOR APPLICATION NUMBER: US 10/131,831
;; PRIOR FILING DATE: 2002-04-24
;; PRIOR APPLICATION NUMBER: US 10/325,899
;; PRIOR FILING DATE: 2002-12-20
;; NUMBER OF SEQ ID NOS: 3117
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 2540
;; LENGTH: 351
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-511-937-2540

Query Match 34.7%; Score 34; DB 6; Length 351;
Best Local Similarity 46.2%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 6 LGSWRF 18
Db 263 LGSWRF 275

RESULT 8
US-10-975-692-2
;; Sequence 2, Application US/10975692
;; Publication No. US20060090221A1
;; GENERAL INFORMATION:
;; APPLICANT: WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION
;; APPLICANT: Browne, John A.
;; APPLICANT: Wallis, James G.
;; APPLICANT: Watts, Jennifer L.
;; TITLE OF INVENTION: DESATURASES AND METHODS OF USING THEM FOR SYNTHESIS OF
;; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS
;; FILE REFERENCE: 4630-58963-02
;; CURRENT APPLICATION NUMBER: US/10/975,692
;; CURRENT FILING DATE: 2004-10-26
;; PRIOR APPLICATION NUMBER: US 09/857,583
;; PRIOR FILING DATE: 2001-08-17
;; PRIOR APPLICATION NUMBER: PCT/US99/28655
;; PRIOR FILING DATE: 1999-12-06
;; PRIOR APPLICATION NUMBER: US 60/111,301
;; PRIOR FILING DATE: 1998-12-07
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO 2
;; LENGTH: 447
;; TYPE: PRT
;; ORGANISM: Caenorhabditis elegans
US-10-975-692-2

Query Match 34.7%; Score 34; DB 6; Length 447;
Best Local Similarity 43.8%; Pred. No. 59;
Matches 7; Conservative 4; Mismatches 5; Indels

Qy 2 IRRLGSIWRFIRAFY 17
 || : | : | : ||
Db 130 IRKILETIFTLEAFY 149

```

RESULT 9
US-10-505-928-543
; Sequence 543, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 543
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-543

```

Query Match 34.7%; Score 34; DB 6; Length 522;
Best Local Similarity 47.1%; Pred. No. 70;
Matches 8; Conservative 3; Mismatches 4; Indels

Qy 3 RRFL--GSIWRFIRAFY 17
||| | : | | | :
Db 473 RRETOSGDLYRHIRKEH 489

RESULT 10
 US-11-169-140-109
 ; Sequence 109, Application US/11169140
 ; Publication No. US20060099150A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
 ; APPLICANT: HOUSTON, Lou, L.
 ; APPLICANT: SHERIDAN, Philip, J.
 ; APPLICANT: HAWLEY, Stephen
 ; APPLICANT: GYNN, Jacqueline, M.
 ; APPLICANT: CHAPIN, Steven
 ; TITLE OF INVENTION: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CE
 ; TITLE OF INVENTION: BARRIERS
 ; FILE REFERENCE: 11474-037-999
 ; CURRENT APPLICATION NUMBER: US/11/169,140
 ; CURRENT FILING DATE: 2005-06-27
 ; PRIOR APPLICATION NUMBER: US 60/267,601
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: US 60/248,819
 ; PRIOR FILING DATE: 2000-11-14
 ; PRIOR APPLICATION NUMBER: US 60/248,478
 ; PRIOR FILING DATE: 2000-11-13
 ; PRIOR APPLICATION NUMBER: US 60/237,929
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: 09/949,039
 ; PRIOR FILING DATE: 2001-09-06
 ; PRIOR APPLICATION NUMBER: 09/969,748
 ; PRIOR FILING DATE: 2001-10-02
 ; NUMBER OF SEQ ID NOS: 143
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 109
 ; LENGTH: 244
 ; TYPE: PRT
 ; ORGANISM: Simian
 US-11-169-140-109

Query Match 34.2%; Score 33.5; DB 7; Length 244;
Best Local Similarity 42.1%; Pred. No. 35;
Matches 8: Conservative 3; Mismatches 3; Indels

Qy 1 GIRRFLGSIW----RFIR 14
|: ||::| ||||
Db 158 GLVLALGAVWCVARARFIR 176

```

RESULT 11
US-11-204-427-7
; Sequence 7, Application US/11204427
; Publication No. US20060100146A1
; GENERAL INFORMATION:
; APPLICANT: Sturley, Stephen L
; APPLICANT: Turkish, Aaron R
; APPLICANT: Billheimer, Jeffrey T
; APPLICANT: Cromley, Debra
; TITLE OF INVENTION: AWAY-RELATED METHODS AND ARTICLES
; FILE REFERENCE: 0575/72796/JPW/AJW/JCS
; CURRENT APPLICATION NUMBER: US/11/204,427
; CURRENT FILING DATE: 2005-08-15
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 7
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-204-427-7

```

Query Match 33.7%; Score 33; DB 7; Length 342;
Best Local Similarity 50.0%; Pred. No. 63;
Matches 5: Conservative 3; Mismatches 2; Indels

Qy 8 SIWRFIRAFY 17
:|:|:|:|:|
Db 84 AIWROLRDPY 93

```

RESULT 12
US-11-304-129-40
; Sequence 40, Application US/11304129
; Publication No. US2006008915A1
; GENERAL INFORMATION:
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: TAKATSU, Yoshihiro
; APPLICANT: WATANABE, Takuya
; APPLICANT: TERRAO, Yasuko
; APPLICANT: SHINTANI, Yasushi
; APPLICANT: HINUMA, Syuji
; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
; FILE REFERENCE: 2762USOP
; CURRENT APPLICATION NUMBER: US/11/304,129
; CURRENT FILING DATE: 2005-12-15
; PRIOR APPLICATION NUMBER: US/10/333,192
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: JP 2000-217442
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: JP 2001-26779
; PRIOR FILING DATE: 2001-09-02
; PRIOR APPLICATION NUMBER: PCT/JP01/06162
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 40
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Rat
US-11-304-129-40

Query Match          33.7%;   Score 33;   DB 7;   Length 393;
Best Local Similarity 46.2%;   Pred. No. 75;

```

Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 FLGSIWRFIRAFY 17

Db 216 FCGQIWPVDQQFY 228

RESULT 13

US-11-304-129-48
; Sequence 48, Application US/11304129
; Publication No. US2006008915A1
; GENERAL INFORMATION:
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: TAKATSU, Yoshihiro
; APPLICANT: WATANABE, Takuya
; APPLICANT: TERAOKA, Yasuko
; APPLICANT: SHINTANI, Yasushi
; APPLICANT: HINUMA, Syuji
; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
; FILE REFERENCE: 2762USOP
; CURRENT APPLICATION NUMBER: US/11/304,129
; CURRENT FILING DATE: 2005-12-15
; PRIOR APPLICATION NUMBER: US/10/333,192
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: JP 2000-217442
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: JP 2001-26779
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/JP01/06162
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 48
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Mouse
US-11-304-129-48

Query Match 33.7%; Score 33; DB 7; Length 393;

Best Local Similarity 46.2%; Pred. No. 75;

Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 FLGSIWRFIRAFY 17

Db 216 FCGQIWPVDQQFY 228

RESULT 14

US-10-505-928-545
; Sequence 545, Application US/10505928
; Publication No. US20060089532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 545
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-545

Query Match 33.7%; Score 33; DB 6; Length 463;

Best Local Similarity 33.3%; Pred. No. 90;

Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 4 RFLGSIWRFIRAFY 18

| : : : |||

Db 339 RYYSSEYHYVGFY 353

RESULT 15

US-10-505-928-853
; Sequence 853, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 853
; LENGTH: 1531
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-853

Query Match 33.7%; Score 33; DB 6; Length 1531;

Best Local Similarity 50.0%; Pred. No. 3.6e+02;

Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 LGSIWRFIRAFY 17

| : : : |||

Db 1122 LGLIYFFVQRFY 1133

Search completed: May 19, 2006, 15:28:17

Job time : 3.14286 secs

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:13:22 ; Search time 94.2857 seconds

(without alignments)
87.287 Million cell updates/sec

Title: US-10-712-447-115

Perfect score: 98

Sequence: 1 GLRRFIGSIWRFIRAFVG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_8.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	98	100.0	18	ADO34338	Ado34338 Synthetic
2	98	100.0	18	ADO34339	Ado34339 Synthetic
3	94	95.9	18	ADO34231	Ado34231 Synthetic
4	94	95.9	18	ADO34354	Ado34354 Synthetic
5	94	95.9	18	ADO34225	Ado34225 Synthetic
6	94	95.9	18	ADO34228	Ado34228 Synthetic
7	94	95.9	18	ADO34236	Ado34236 Synthetic
8	94	95.9	18	ADO34340	Ado34340 Synthetic
9	94	95.9	18	ADO34233	Ado34233 Synthetic
10	94	95.9	18	ADO34350	Ado34350 Synthetic
11	91	92.9	18	ADO34314	Ado34314 Synthetic
12	90	91.8	18	ADO34352	Ado34352 Synthetic
13	88	89.8	18	ADO34297	Ado34297 Synthetic
14	88	89.8	18	ADO34244	Ado34244 Synthetic
15	88	89.8	18	ADO34276	Ado34276 Synthetic
16	86	87.8	18	ADO34227	Ado34227 Synthetic
17	86	87.8	18	ADO34335	Ado34335 Synthetic
18	85	86.7	18	ADO34322	Ado34322 Synthetic
19	84	85.7	18	ADO34336	Ado34336 Synthetic
20	84	85.7	18	ADO34337	Ado34337 Synthetic
21	84	85.7	18	ADO34241	Ado34241 Synthetic
22	83	84.7	18	ADO34240	Ado34240 Synthetic
23	83	84.7	18	ADO34344	Ado34344 Synthetic

24	82	83.7	18	8	ADO34284	Ado34284 Synthetic
25	82	83.7	18	8	ADO34305	Ado34305 Synthetic
26	81	82.7	18	8	ADO34239	Ado34239 Synthetic
27	81	82.7	18	8	ADO34319	Ado34319 Synthetic
28	80	81.6	18	8	ADO34245	Ado34245 Synthetic
29	80	81.6	18	8	ADO34301	Ado34301 Synthetic
30	80	81.6	18	8	ADO34343	Ado34343 Synthetic
31	80	81.6	18	8	ADO34318	Ado34318 Synthetic
32	78	79.6	18	8	ADO34302	Ado34302 Synthetic
33	78	79.6	18	8	ADO34279	Ado34279 Synthetic
34	78	79.6	18	8	ADO34303	Ado34303 Synthetic
35	78	79.6	18	8	ADO34242	Ado34242 Synthetic
36	78	79.6	18	8	ADO34300	Ado34300 Synthetic
37	78	79.6	18	8	ADO34281	Ado34281 Synthetic
38	78	79.6	18	8	ADO34317	Ado34317 Synthetic
39	77	78.6	18	8	ADO34323	Ado34323 Synthetic
40	77	78.6	18	8	ADO34280	Ado34280 Synthetic
41	76	77.6	18	8	ADO34264	Ado34264 Synthetic
42	76	77.6	18	8	ADO34342	Ado34342 Synthetic
43	75	76.5	18	8	ADO34320	Ado34320 Synthetic
44	74	75.5	18	2	AAV18917	AAV18917 Lecithin:
45	74	75.5	18	2	AAV19171	AAV19171 Lecithin:

ALIGNMENTS

RESULT 1
ADO34338
ID ADO34338 standard; peptide; 18 AA.
XX
AC ADO34338;
XX
DT 12-AUG-2004 (first entry)
XX
DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 115.
XX
KW apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;
KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.
XX
OS Synthetic.
XX
PN WO2004043403-A2.
XX
PD 27-MAY-2004.
XX
PF 13-NOV-2003; 2003WO-US036268.
XX
PR 13-NOV-2002; 2002US-0425821P.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Anantharamiah GM, Garber DW, Datta G;
XX
DR WPI; 2004-411629/38.
XX
PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
PT comprises an amino acid sequence.
XX
PS Claim 4; SEQ ID NO 115; 79pp; English.
XX
CC The invention relates to a novel synthetic apolipoprotein-E mimicking
CC polypeptide. The invention further comprises an isolated nucleic acid
CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
CC a host cell, a recombinant cell or a transgenic, non-human subject
CC (including animal or plant) comprising the synthetic apolipoprotein-E
CC mimicking polypeptide encoding polynucleotide; a composition comprising
CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
CC an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC myocardial infarction or atherosclerosis; and for reducing the risk of
 CC also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5.2e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRRFIGSIWRFFIRAFYG 18
 |||||
 Db 1 GLRRFIGSIWRFFIRAFYG 18

RESULT 2

ADO34339
 ID ADO34339 standard; peptide; 18 AA.

XX AC ADO34339;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 116.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 116; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5.2e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRRFIGSIWRFFIRAFYG 18
 |||||
 Db 1 GLRRFIGSIWRFFIRAFYG 18

RESULT 3

ADO34231
 ID ADO34231 standard; peptide; 18 AA.

XX AC ADO34231;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 8.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 8; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,

xx The invention relates to a novel synthetic apolipoprotein-E mimicking
 cc polypeptide. The invention further comprises an isolated nucleic acid
 cc encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 cc encoding the synthetic apolipoprotein-E mimicking polypeptide; a cell,
 cc a host cell, a recombinant cell or a transgenic, non-human subject
 cc comprising the synthetic apolipoprotein-E mimicking polypeptide;
 cc (including animal or plant) comprising the synthetic apolipoprotein-E
 cc mimicking polypeptide encoding polynucleotide; a composition comprising
 cc the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 cc an monoclonal antibody that specifically binds to the synthetic
 cc apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 cc mimicking polypeptide has the following activities: antilipemic,
 cc cardiatic, vasotonic, antiatherosclerotic, cerebroprotective, and
 cc antitumor.

xx The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector
 CC comprising the synthetic apolipoprotein-E mimicking polypeptide; a host cell,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide; a composition comprising

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;
 SQ

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.1e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRFIRAFYG 18
 |:||||:||||:||||:
 Db 1 GIRRFGLSIWRFIRAFYG 18

RESULT 8
 ADO34340
 ID ADO34340 standard; peptide; 18 AA.

XX ADO34340;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 117.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 117; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.1e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRFIRAFYG 18
 |:||||:||||:||||:
 Db 1 GIRRFGLSIWRFIRAFYG 18

RESULT 9
 ADO34233
 ID ADO34233 standard; peptide; 18 AA.

XX ADO34233;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 10.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 10; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,

CC useful for reducing serum cholesterol in a subject (including a mammal
CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
CC chimpanzee or orangutan); for treating coronary artery disease,
CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
CC myocardial infarction or stroke; for breaking an embolus in the subject;
CC and also for treating angina. The synthetic apolipoprotein-E mimicking
CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 92.9%; Score 91; DB 8; Length 18;

Best Local Similarity 83.3%; Pred. No. 6.2e-07;

Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRPIAFYG 18

Db 1 GIRKPLGSIWRPIAFYG 18

RESULT 12

ADO34352

ID ADO34352 standard; peptide; 18 AA.

XX AC ADO34352;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 129.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;

XX KW vasotrophic; antiarteriosclerotic; cerebroprotective; antianginal;

XX KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;

XX KW atherosclerosis; myocardial infarction; stroke; embolus; angina;

XX KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating

XX PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis

XX PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 129; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking
XX CC polypeptide. The invention further comprises an isolated nucleic acid
XX CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
XX CC a host cell, a recombinant cell or a transgenic, non-human subject
XX CC (including animal or plant) comprising the synthetic apolipoprotein-E
XX CC mimicking polypeptide encoding polynucleotide; a composition comprising
XX CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
XX CC an monoclonal antibody that specifically binds to the synthetic
XX CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
XX CC mimicking polypeptide has the following activities: antilipaeamic,
XX CC cardiant, vasotrophic, antiarteriosclerotic, cerebroprotective, and
XX CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
XX CC useful for reducing serum cholesterol in a subject (including a mammal

CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
CC chimpanzee or orangutan); for treating coronary artery disease,
CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
CC myocardial infarction or stroke; for breaking an embolus in the subject;
CC and also for treating angina. The synthetic apolipoprotein-E mimicking
CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 91.8%; Score 90; DB 8; Length 18;

Best Local Similarity 77.8%; Pred. No. 8.9e-07;

Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRPIAFYG 18

Db 1 GIRKPLGSIWRPIAFYG 18

RESULT 13

ADO34297

ID ADO34297 standard; peptide; 18 AA.

XX AC ADO34297;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 74.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;

XX KW vasotrophic; antiarteriosclerotic; cerebroprotective; antianginal;

XX KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;

XX KW atherosclerosis; myocardial infarction; stroke; embolus; angina;

XX KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating

XX PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis

XX PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 74; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking
XX CC polypeptide. The invention further comprises an isolated nucleic acid
XX CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
XX CC a host cell, a recombinant cell or a transgenic, non-human subject
XX CC (including animal or plant) comprising the synthetic apolipoprotein-E
XX CC mimicking polypeptide encoding polynucleotide; a composition comprising
XX CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
XX CC an monoclonal antibody that specifically binds to the synthetic
XX CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
XX CC mimicking polypeptide has the following activities: antilipaeamic,
XX CC cardiant, vasotrophic, antiarteriosclerotic, cerebroprotective, and
XX CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
XX CC useful for reducing serum cholesterol in a subject (including a mammal

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and a monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antiangiinal. The synthetic apolipoprotein-E mimicking polypeptide is

CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 SQ Sequence 18 AA;

Query Match 89.8%; Score 88; DB 8; Length 18;
 Best Local Similarity 77.8%; Pred. No. 1.8e-06;
 Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GLRFFIGSIWRFIRAFYG 18
 |::|:|||||:|
 Db 1 GIKRFLGSIWRFIRAFYG 18

Search completed: May 19, 2006, 14:24:31
 Job time : 94.2857 secs

This Page Blank (uspto)

Result No.	Score	Query Match	Length	DB	ID	Description
1	48	49.0	627	2	S76462	hypothetical prote
2	47	48.0	516	2	T33269	hypothetical prote
3	45	45.9	489	2	B84733	probable cytochrom
4	44	44.9	246	2	I54412	MHC HLA-A cell sur
5	44	44.9	273	1	HLHU69	MHC class I histoc
6	44	44.9	365	2	IHLUA2	MHC class I histoc
7	44	44.9	365	2	I38443	gene HLA-A-0203 pr
8	44	44.9	365	2	I61902	MHC class I histoc
9	44	44.9	365	2	I37542	MHC class I histoc
10	44	44.9	365	2	I84448	MHC class I histoc
11	44	44.9	365	2	I61857	MHC HLA-A2.4a chai
12	44	44.9	589	2	I38442	gene HLA-A-0205 pr
13	44	44.9	589	2	A34341	poly (3-hydroxybuty
14	43	43.9	503	2	B81690	probable sodium-tr
15	43	43.9	519	1	T02263	cytochrome P450 DW
16	42.5	43.4	760	2	B84953	penicillin-binding
17	42	42.9	119	2	G64032	hypothetical prote
18	42	42.9	214	2	D72540	hypothetical prote
19	42	42.9	237	2	B72892	hypothetical prote
20	42	42.9	537	2	T04745	hypothetical prote
21	42	42.9	785	2	S63652	leucyl-tRNA synthet
22	42	42.9	806	2	A84060	leucine-tRNA ligase
23	42	42.9	861	2	H64102	probable calcium-a
24	42	42.9	1112	2	T42383	acridinase
25	41.5	42.3	1025	2	AH3568	transcription regul
26	41	41.8	178	2	A75578	hypothetical prote
27	41	41.8	265	2	T32316	rfap protein - bac
28	41	41.8	265	2	C42595	hypothetical prote
29	41	41.8	359	2	T20575	hypothetical prote

Nature 357, 326-329, 1992
A;Title: Unusual HLA-B alleles in two tribes of Brazilian Indians.
A;Reference number: I37120; MUID:92289955; PMID:1317015
A;Accession: S77965
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-365 <BBL>
A;Cross-references: UNIPARC:UPI0000124E24; EMBL:M84379; NID:G403143; PIDN:AAA59606.1; PII
A;Experimental source: cell line GRC 138; isolate A*0201
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
R;Castano, A.R.; Lopez de Castro, J.A.
Immunogenetics 35, 344-346, 1992
A;Title: Structure of the HLA-A *0211 (A2.5) subtype: further evidence for selection-driven
A;Reference number: S23593; MUID:92218010; PMID:1559719
A;Accession: S23593
A;Molecule type: mRNA
A;Residues: 9-96, 'ID', 99-365 <CAS2>
A;Cross-references: UNIPARC:UPI000008AF57; EMBL:X60764; NID:G32156; PIDN:CAB56609.1; PII
A;Note: this allele is designated A*0211 (previously HLA-A2.5)
R;Orr, H.T.; Lopez de Castro, J.A.; Parham, P.; Ploegh, H.L.; Strominger, J.L.
Proc. Natl. Acad. Sci. U.S.A. 76, 4395-4399, 1979
A;Title: Comparison of amino acid sequences of two human histocompatibility antigens, HL
A;Reference number: A93834; MUID:80056745; PMID:92029
A;Accession: A93834
A;Molecule type: protein
A;Residues: 25-55, 'Z', 57-60, 'B', 62, 'B', 64-66, 'Z', 68-74, 'X', 76-85, 'RXXX', 90-94, 'AH', 97, 'V'
A;Cross-references: UNIPARC:UPI00001737EE
A;Note: this sequence has been revised in reference A93919
R;Lopez de Castro, J.A.; Strominger, J.L.; Strong, D.M.; Orr, H.T.
Proc. Natl. Acad. Sci. U.S.A. 79, 3813-3817, 1982
A;Title: Structure of crossreactive human histocompatibility antigens HLA-A28 and HLA-A2
A;Reference number: A93919; MUID:82247941; PMID:6179086
A;Accession: A93919
A;Molecule type: protein
A;Residues: 25-85, 'RXXX', 90-94, 'AH', 97, 'V', 99-112, 'Z', 114-118, 'LZ', 121-125, 'X', 127-131, '
'232-265, 'E', 267-294 <LOP>
A;Cross-references: UNIPARC:UPI00001737EF
R;Silver, M.L.; Parker, K.C.; Wiley, D.C.
Nature 350, 619-622, 1991
A;Title: Reconstitution by MHC-restricted peptides of HLA-A2 heavy chain with beta-2-mic
A;Reference number: S14802; MUID:91204056; PMID:2017257
A;Accession: S14802
A;Molecule type: protein
A;Residues: 25-36 <SLI>
A;Cross-references: UNIPARC:UPI00001737F0
C;Genetics:
A;Gene: GDB:HLA-A
A;Cross-references: GDB:119310; OMIM:142800
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterodimer; transmembrane protein; transplantati
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-365/Product: MHC class I histocompatibility antigen HLA-A2 alpha chain #status expe
F;25-114/Domain: alpha-1 <EX1>
F;115-206/Domain: alpha-2 <EX2>
F;220-285/Domain: immunoglobulin homology <IMM>
F;307-331/Domain: transmembrane #status predicted <TM>
F;332-365/Domain: intracellular #status predicted <INT>
F;110/Binding site: carbohydrate (Aen) (covalent) #status experimental
F;125-188,227-283/Disulfide bonds: #status predicted

Query Match 44.9%; Score 44; DB 1; Length 365;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 6 IGSWRFIRAFY 17
DB 127 VGSDWRFRLRGYH 138
RESULT 7
138443

gene HLA-A-0203 protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
A;Reference number: I37120; MUID:92289955; PMID:1317015
A;Accession: I38443
R;Holmes, N.; Ennis, P.; Wan, A.M.; Denney, D.W.; Parham, P.
J. Immunol. 139, 936-941, 1987
A;Title: Multiple genetic mechanisms have contributed to the generation of the HLA-A2/A28
A;Reference number: I38441; MUID:87252273; PMID:3496393
A;Accession: I38443
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-365 <RES>
A;Cross-references: UNIPARC:UPI000016A05E; EMBL:U03863; NID:G432438; PIDN:AAA03604.1; PII
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 44.9%; Score 44; DB 2; Length 365;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 6 IGSWRFIRAFY 17
DB 127 VGSDWRFRLRGYH 138
RESULT 8
161902
MHC class I histocompatibility antigen HLA-A alpha chain precursor - human (isolate A*021
C;Species: Homo sapiens (man)
A;Variety: isolate A*0212
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 23-Jul-1999
C;Accession: I61902
R;Balich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.; I
Nature 357, 326-329, 1992
A;Title: Unusual HLA-B alleles in two tribes of Brazilian Indians.
A;Reference number: I37120; MUID:92289955; PMID:1317015
A;Accession: I61902
A;Molecule type: mRNA
A;Status: translated from GB/EMBL/DBJ
A;Residues: 1-365 <RES>
A;Cross-references: UNIPARC:UPI000016AD39; db:M84378; NID:G187625; PIDN:AAA59604.1; PII:
A;Experimental source: cell line KRC 033; isolate A*0212
C;Genetics:
A;Gene: GDB:HLA-A
A;Cross-references: GDB:119310; OMIM:142800
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-365/Product: MHC class I histocompatibility antigen HLA-A alpha chain #status predic
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 44.9%; Score 44; DB 2; Length 365;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 6 IGSWRFIRAFY 17
DB 127 VGSDWRFRLRGYH 138
RESULT 9
137542
MHC class I histocompatibility antigen HLA-A2 alpha chain (allele A*0216) precursor - hun
C;Species: Homo sapiens (man)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C;Accession: I37542; S49582
R;Barouch, D.; Krausa, P.; Bodmer, J.; Browning, M.J.; McMichael, A.J.
Immunogenetics 41, 388, 1995
A;Title: Identification of a novel HLA-A2 subtype, HLA-A*0216.
A;Reference number: I37542; MUID:95278976; PMID:7759139
A;Accession: I37542
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA
A;Residues: 1-365 <RES>
A;Cross-references: UNIPARC:UPI000016AA63; EMBL:Z46633; NID:G575248; PIDN:CAA86602.1; PID:
A;Note: submitted to the EMBL Data Library, November 1994
C;Genetics:
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 44.9%; Score 44; DB 2; Length 365;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSIRWFIRAFY 17
: || ||| : : :
Db 127 VGSDWRFRLRGYH 138

RESULT 10

I84448
MHC class I histocompatibility antigen HLA-A alpha chain precursor - human (isolate A*0211)
C;Species: Homo sapiens (man)
A;Variety: isolate A*0211
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999
C;Accession: I84448
R;Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.;
Nature 357, 326-329, 1992
A;Title: Unusual HLA-B alleles in two tribes of Brazilian Indians.
F;1-24/Domain: signal sequence
A;Reference number: I37120; MUID:92269955; PMID:1317015
A;Accession: I84448
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-365 <RES>
A;Cross-references: UNIPARC:UPI000016AD38; GB:M84377; NID:G187623; PIDN:AAAS9603.1; PID:
A;Experimental source: cell line GRC 138; isolate A*0211
C;Genetics:
A;Gene: GDB:HLA-A
A;Cross-references: GDB:119310; OMIM:142800
A;Map position: gp21.3-gp21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: transmembrane protein
F;1-24/Domain: signal sequence
F;25-365/Product: MHC class I histocompatibility antigen HLA-A alpha chain #status predicted
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 44.9%; Score 44; DB 2; Length 365;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSIRWFIRAFY 17
: || ||| : : :
Db 127 VGSDWRFRLRGYH 138

RESULT 11

I61857
MHC HLA-A2.4a chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I61857
R;Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
J. Immunol. 142, 3937-3950, 1989
A;Title: Diversity and diversification of HLA-A,B,C alleles.
A;Reference number: I36956; MUID:89235215; PMID:2715640
A;Accession: I61857
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-365 <RES>
A;Cross-references: UNIPROT:P01892; UNIPARC:UPI000016AD48; GB:M24042; NID:G187777; PIDN:
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 44.9%; Score 44; DB 2; Length 365;

Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSIRWFIRAFY 17
: || ||| : : :
Db 127 VGSDWRFRLRGYH 138

RESULT 12

I38442
gene HLA-A-0205 protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I38442
R;Holmes, N.; Ennis, P.; Wan, A.M.; Denney, D.W.; Parham, P.
J. Immunol. 139, 936-941, 1987
A;Title: Multiple genetic mechanisms have contributed to the generation of the HLA-A2/A28
A;Reference number: I38441; MUID:87252273; PMID:3496393
A;Accession: I38442
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-365 <RES>
A;Cross-references: UNIPROT:P01892; UNIPARC:UPI000016A06D; EMBL:U03862; NID:G432436; PIDN:
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 44.9%; Score 44; DB 2; Length 365;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSIRWFIRAFY 17
: || ||| : : :
Db 127 VGSDWRFRLRGYH 138

RESULT 13

A34341
poly(3-hydroxybutyrate) synthase (EC 2.3.1.-) - Alcaligenes eutrophus
C;Species: Alcaligenes eutrophus
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C;Accession: A34341; A39190
R;Peoples, O.P.; Sinskey, A.J.
J. Biol. Chem. 264, 15298-15303, 1989
A;Title: Poly-beta-hydroxybutyrate (PHB) biosynthesis in Alcaligenes eutrophus H16. Ident
A;Reference number: A34341; MUID:89359357; PMID:2670936
A;Accession: A34341
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-589 <PEO>
A;Cross-references: UNIPROT:P23608; UNIPARC:UPI0000044953; GB:J05003; NID:G141958; PIDN:
A;Experimental source: strain H16
R;Schubert, P.; Krueger, N.; Steinbuechel, A.
J. Bacteriol. 173, 168-175, 1991
A;Title: Molecular analysis of the Alcaligenes eutrophus poly(3-hydroxybutyrate) biosynt
omoter.
A;Reference number: A39190; MUID:91100279; PMID:1987116
A;Accession: A39190
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-219 <SCH>
A;Cross-references: UNIPARC:UPI000016E162; GB:M64341; NID:G141964; PIDN:AAA21979.1; PID:
A;Note: the authors translated the codon TAC for residue 120 as Thr
C;Superfamily: poly(3-hydroxyalkanoic acid) synthase phbc
C;Keywords: acyltransferase

Query Match 44.9%; Score 44; DB 2; Length 589;
Best Local Similarity 47.6%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

QY 3 RRFSGSIW-----RIRAFY 17
||| ||| |||
Db 100 RRFAGDAWRNLNLPYRFAAFY 120

Search completed: May 19, 2006, 14:39:58
Job time : 14.2857 secs

This Page Blank (uspto)

GenCore version 5.1.8
 Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:13:32 ; Search time 115.429 Seconds
 (without alignments)
 144.247 Million cell updates/sec

Title: US-10-712-447-115
 Perfect score: 98
 Sequence: 1 GLRRFIGSIWRFRFYG 18

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 40 summaries

Database : Uniprot 7.2.*
 1: uniprot_sprot.*
 2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	55.1	670	2 Q25271 LRPDE	Q25271 leptinotars
2	54	55.1	805	2 Q3APY5 CHLCH	Q3APY5 chlorobium
3	51	52.0	488	2 Q84ZW1 PEA	Q84ZW1 pisum sativ
4	50	51.0	735	2 Q9F7V7 RHILV	Q9F7V7 rhizobium l
5	48	49.0	361	2 Q2N8U5 SODGL	Q2N8U5 sodalis glo
6	48	49.0	401	2 Q7NKK3 GLOVI	Q7NKK3 gloeobacter
7	48	49.0	449	2 Q3PK79 PARDE	Q3PK79 paracoccus
8	48	49.0	579	1 XKR7 HUMAN	Q5gh72 homo sapien
9	48	49.0	579	1 XKR7 PANTR	Q43l81 pan troglod
10	48	49.0	580	1 XKR7 MOUSE	Q5gh64 mus musculu
11	48	49.0	580	1 XKR7 RAT	Q5gh56 rattus norv
12	48	49.0	597	2 Q5AUS5 EMENI	Q5aus5 aspergillus
13	48	49.0	627	2 P74489 SVNY3	P74489 synchocyst
14	48	49.0	805	2 Q44QD1 CHLLI	Q44qd1 chlorobium
15	48	49.0	816	2 Q43K01 9CHLB	Q43k01 chlorobium
16	47	48.0	219	2 Q6LIT5 PICTO	Q6llt5 picrophilus
17	47	48.0	287	2 Q76442 CABEL	Q76442 caenorhabdi
18	47	48.0	407	2 Q39L57 BURS3	Q39l57 burkholderi
19	47	48.0	408	2 Q456F4 9BURK	Q456f4 burkholderi
20	47	48.0	408	2 Q4LK44 9BURK	Q4lk44 burkholderi
21	47	48.0	486	2 Q5U4I4 XENLA	Q5u4i4 xenopus lae
22	47	48.0	487	2 Q3ZN49 XENLA	Q3zn49 xenopus lae
23	47	48.0	506	2 Q5VRM7 ORISA	Q5vrm7 oryza sativ
24	47	48.0	607	2 Q425W5 DESHA	Q425w5 desulfitoba
25	46	46.9	426	2 Q99A07 9VIRU	Q99aq7 torque teno
26	46	46.9	578	1 XKB6 TETNG	Q49l88 tetraodon n
27	46	46.9	578	2 Q5GH49 FUGRU	Q5gh49 fugu rubrip
28	46	46.9	836	2 Q2Y8V4 NITMU	Q2y8v4 nitrosospir
29	45	45.9	278	2 Q7VV93 BORPE	Q7vv93 bordetella
30	45	45.9	278	2 Q7WP3 BORPA	Q7wp3 bordetella
31	45	45.9	278	2 Q7WL31 BORBR	Q7wl31 bordetella

32	45	45.9	376	2 Q8KBA7 CHLTE	Q8kba7 chlorobium
33	45	45.9	406	2 Q56YS1 ARATH	Q56ys1 arabidopsis
34	45	45.9	409	2 Q4BFM2 BURVI	Q4bfm2 burkholderi
35	45	45.9	435	2 Q2JIT0 9CYAN	Q2jit0 cyanobacter
36	45	45.9	458	2 Q3M6C5 ANAVT	Q3m6c5 anabaena va
37	45	45.9	458	2 Q8XG08 TALSO	Q8xg08 ralsstonia s
38	45	45.9	489	1 KAO2 ARATH	Q8c5y2 arabidopsis
39	45	45.9	490	2 Q84ZW0 PEA	Q84zw0 pisum sativ
40	45	45.9	513	2 Q00857 FUSSP	Q00857 fusarium sp
41	45	45.9	519	2 Q9CIB7 FUSSP	Q9cib7 fusarium sp
42	45	45.9	540	2 Q5GH65 MOUSE	Q5gh65 mus musculu
43	45	45.9	580	2 Q5GH40 BRARE	Q5gh40 brachydanio
44	45	45.9	638	1 XKR6 RAT	Q5gh57 rattus norv
45	45	45.9	641	1 XKR6 HUMAN	Q5gh73 homo sapien

ALIGNMENTS

RESULT 1
 Q25271 LRPDE
 ID Q25271_LRPDE PRELIMINARY; PRT; 670 AA.
 AC Q25271, 1996, integrated into UniProtKB/TREMBL.
 DT 01-NOV-1996, sequence version 1.
 DT 07-FEB-2006, entry version 25.
 DE Diapause protein 1 (Fragment).
 GN Name=Dp19;
 OS Leptinotarsa decemlineata (Colorado potato beetle).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Chrysomeloidea; Chrysomelidae; Chrysomelinae; Doryphorini;
 OC Leptinotarsa.
 OC NCBI_TaxID=7539;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA de Kort C.A.D., Koopmanschap A.B.;
 RT "Nucleotide and deduced amino acid sequence of a cDNA clone encoding
 RT diapause protein 1, an amylophorin-type storage hexamer of the Colorado
 RT potato beetle.";
 RL J. Insect Physiol. 40:527-535 (1994).
 CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
 CC Distributed under the Creative Commons Attribution-NoDerivs License

EMBL; X76080; CAA53691.1; -; mRNA.
 HSSP; P04253; 1LL1.
 GO; GO:0005344; P:oxygen transporter activity; IEA.
 GO; GO:0006810; P:transport; IEA.
 InterPro; IPR000896; Hemocyanin.
 InterPro; IPR005203; hemocyanin C.
 InterPro; IPR005204; hemocyanin N.
 PANTHER; PTHR11511; Hemocyanin; 1.
 Pfam; PF03723; Hemocyanin_C; 1.
 Pfam; PF03772; Hemocyanin_M; 1.
 Pfam; PF03722; Hemocyanin_N; 1.
 PRINTS; PR00187; HAEMOCYANIN.
 PROSITE; PS00210; HEMOCYANIN_2; UNKNOWN_1.
 NON TER 1
 SEQUENCE 670 AA; 79825 MW; 8A000BA115BEC8A6 CRC64;

Query Match 55.1%; Score 54; DB 2; Length 670;

Best Local Similarity 43.8%; Pred. No. 9.8;

Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 3 RRFIGSIWRFRFYG 18

| | | | | | | | | |

Db 351 RKFYGALMSYLRHFFG 366

RESULT 2

Q3APY5 CHLCH

ID Q3APY5_CHLCH PRELIMINARY; PRT; 805 AA.

DR	GO: 0006118; P-electron transport; IEA.
DR	InterPro; IPRO01128; Cytochrome_P450.
DR	InterPro; IPRO02401; EP4501.
DR	PANTHER; PTHR19383; Cytochrome_P450; 1.
DR	Pfam; PF00067; p450; 2.
DR	PRINTS; PR00463; EP4501.
DR	PRINTS; PR00385; P450.
DR	PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW	Endoplasmic reticulum; Heme; Iron; Membrane; Metal-binding;
KW	Monooxygenase; Oxidoreductase.
SQ	SEQUENCE 488 AA; 56478 MW; 503453CB6E43C830 CRC64;
Query Match 52.0%; Score 51; DB 2; Length 488;	
Best Local Similarity 66.7%; Pred. No. 21;	
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps	
Qy	5 FIGSIWRFIRAF 16 : : :
Dd	54 FIGNMFSLRAF 65 : : :
RESULT 4	
Q9F7V7 RHILV	PRELIMINARY; PRT; 735 AA.
AC	Q9F7V7;
DT	01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT	01-MAR-2001, sequence version 1.
DT	07-FEB-2006, entry version 25.
DE	ABC transporter Rzcb.
GN	Name=rzcb;
OS	Rhizobium leguminosarum bv. viciae.
OC	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC	Rhizobiaceae; Rhizobium.
OX	NCBI_TaxID=387;
RP	[1]
RN	NUCLEOTIDE SEQUENCE.
RC	STRAIN=305;
RC	MEDLINE=21360352; PubMed=11467725; DOI=10.1139/cjm-47-6-495;
RT	Venter A.P., Twelker S., Oresnik I.J., Hynes M.F.;
RT	"Analysis of the genetic region encoding a novel rhizobiocin from
RT	Rhizobium leguminosarum bv. viciae strain 305.";
RL	Can. J. Microbiol. 47:495-502(2001).
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC	Distributed under the Creative Commons Attribution-NoDerivs License
CC	EMBL; AF273216; AAC25076.1; -; Genomic_DNA.
DR	HSPSP; P08716; IMT0
DR	GO: 0016021; C-integral to membrane; IEA.
DR	GO: 0005524; F-ATP binding; IEA.
DR	GO: 0016887; F-ATPase activity; IEA.
DR	GO: 0042626; F-ATPase activity, coupled to transmembrane m. .; IEA
DR	GO: 0000166; F-nucleotide binding; IEA.
DR	GO: 0008233; F-peptidase activity; IEA.
DR	GO: 0008565; F-protein transporter activity; IEA.
DR	GO: 0015031; P-protein transport; IEA.
DR	GO: 0006508; P-proteolysis; IEA.
DR	InterPro; IPRO03593; AAA_ATPase.
DR	InterPro; IPRO11527; ABC_TM_1.
DR	InterPro; IPRO01140; ABC_TM_transpt.
DR	InterPro; IPRO03439; ABC_transp.like.
DR	InterPro; IPRO05074; Peptidase_C39
DR	InterPro; IPRO10132; Type_I_sec_HlyB.
DR	PANTHER; PTHR19242:SF74; Type_I_sec_HlyB; 1.
DR	Pfam; PF00664; ABC membrane; 1.
DR	Pfam; PF00005; ABC_tran; 1.
DR	Pfam; PF03412; Peptidase_C39; 1.
DR	ProDom; PD000006; ABC transporter; 1.
DR	SMART; SM00382; AAA; 1.
DR	TIGRFAMS; TIGR01846; type_I_sec_HlyB; 1.
DR	PROSITE; PS50929; ABC_TMIF; 1.
DR	PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR	PROSITE; PS50893; ABC_TRANSPORTER_2; 1.

```
DR PROSITE; PS0990; PEPTIDASE C39; 1.
SQ SEQUENCE 735 AA; 80717 MW; 0216259241F3630C CRC64;

Query Match 51.0%; Score 50; DB 2; Length 735;
Best Local Similarity 56.2%; Pred. No. 47;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 GLRRFIGSIWRFIRAF 16
DB 161 GFRWFLPAIWRYRRAP 176

RESULT 5
Q2NUB5 SODGL
ID Q2NUB5 SODGL PRELIMINARY; PRT; 361 AA.
AC Q2NUB5;
DT 07-FEB-2006, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DT 07-MAR-2006, entry version 2.
DE Putative glycosyltransferase.
GN ORFNames=SG0985;
OS Sodalis glossinidius str. 'morsitans'.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Sodalis.
OX NCBI_TaxID=343509;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Morsitans;
RA Toh H., Weiss B.B., Perkin S.A.H., Yamashita A., Oshima K.,
RA Hattori M., Aksoy S.;
RA "Massive genome erosion and functional adaptations provide insights
RT into the symbiotic lifestyle of Sodalis glossinidius in the tsetse
RT host.";
RL Genome Res. 16:149-156(2006).
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AP008232; BAE74260.1; -; Genomic_DNA.
KW Transferase.
SQ SEQUENCE 361 AA; 40247 MW; 1557F70F3C3CA6EC CRC64;

Query Match 49.0%; Score 48; DB 2; Length 361;
Best Local Similarity 61.5%; Pred. No. 47;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 RFIGSIWRFIRAF 16
DB 62 RDVGFWRFILSAF 74

RESULT 6
Q7NWK3 GLOVI
ID Q7NWK3 GLOVI PRELIMINARY; PRT; 401 AA.
AC Q7NWK3;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Gll1363 protein.
GN OrderedLocusNames=gll1363;
OS Gloeobacter violaceus.
OC Bacteria; Cyanobacteria; Gloeobacteria; Gloeobacteriales; Gloeobacter.
OX NCBI_TaxID=33072;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=PCC 7421;
RX MEDLINE=22977040; PubMed=14621292; DOI=10.1093/dnares/10.4.137;
RA Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,
RA Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpō S.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a
RT cyanobacterium that lacks thylakoids.";
```

```
RL DNA Res. 10:137-145(2003).
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; BA000045; BAC89304.1; -; Genomic_DNA.
DR BioCyc; GVIO251221:GLU1363-MONOMER; -.
DR GO; GO:0004040; F:amidase activity; IEA.
DR GO; GO:0008745; F:N-acetylmuramoyl-L-alanine amidase activity; IEA.
DR GO; GO:0009253; P:peptidoglycan catabolism; IEA.
DR InterPro; IPR002508; Amidase_3_hydro.
DR InterPro; IPR002901; Amidase_4.
DR Pfam; PF01520; Amidase_3; 1.
DR Pfam; PF01832; Glucosaminidase; 1.
KW Complete proteome.
SQ SEQUENCE 401 AA; 44051 MW; 903814BB688C170B CRC64;

Query Match 49.0%; Score 48; DB 2; Length 401;
Best Local Similarity 69.2%; Pred. No. 52;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GLRRFIGSIWRFI 13
DB 104 GLERFIRGYWRFI 116

RESULT 7
Q3PK79 PARDE
ID Q3PK79 PARDE PRELIMINARY; PRT; 449 AA.
AC Q3PK79;
DT 25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Cytochrome P450.
GN ORFNames=PdenDRAFT_4722;
OS Paracoccus denitrificans PD1222.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacteriales;
OC Rhodobacteraceae; Paracoccus.
OX NCBI_TaxID=318586;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PD1222;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Paracoccus denitrificans PD1222.";
RT Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
CC CC CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC
CC -! SIMILARITY: Belongs to the cytochrome P450 family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AA101000001; EAG68115.1; -; Genomic_DNA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002401; EP4501.
DR Pfam; PF00067; p450; 1.
DR
```

```

DR PRINTS; PR00463; EP450I.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 449 AA; 50659 MW; 5F3EBC9E12AA3B35 CRC64;

Query Match 49.0%; Score 48; DB 2; Length 449;
Best Local Similarity 80.0%; Pred. No. 59;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 GSIWRFIRAF 16
   |||||
Db 13 GSVRFIRDF 22

RESULT 8
XKR7 HUMAN
ID XKR7 HUMAN STANDARD; PRT; 579 AA.
AC QSGH72; Q9NUG5;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE XK-related protein 7.
GN Name=XKR7; Synonyms=C20orf159, XRG7;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Huang C.-H.; Chen Y.;
RT "A superfamily of XK-related genes (XRG) widely expressed in
RT vertebrates and invertebrates."
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A.G., Coville G.J., Deadman R., Dhali P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grahm D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehaeslao M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Shira H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulten J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20."
RL Nature 414:865-871(2001).
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -!- SIMILARITY: Belongs to the XK family.
CC -!- SIMILARITY: Belongs to the XK family.
CC Copyrighted under the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC gene model prediction.

```

```

CC -----
DR ENBL; AV532425; AAT07094.1; -; mRNA.
DR ENBL; AL031658; CAB88102.1; ALT_SEQ; Genomic_DNA.
DR Ensembl; ENSG00000101321; Homo sapiens.
DR HGNC; HGNC:23062; XKR7.
KW Membrane; Transmembrane.
FT CHAIN 1 579 XK-related protein 7.
FT TRANSMEM 59 79 /FTId=PRO_0000190788.
FT TRANSMEM 89 109 Potential.
FT TRANSMEM 260 280 Potential.
FT TRANSMEM 314 334 Potential.
FT TRANSMEM 355 375 Potential.
FT TRANSMEM 384 404 Potential.
FT TRANSMEM 415 435 Potential.
SQ SEQUENCE 579 AA; 63826 MW; D8D0FF64B9EDD53D CRC64;

Query Match 49.0%; Score 48; DB 1; Length 579;
Best Local Similarity 50.0%; Pred. No. 77;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSWRFIRAF 17
   :||:|
Db 190 LGQWRYLRALY 201

RESULT 9
XKR7 PANTR
ID XKR7 PANTR STANDARD; PRT; 579 AA.
AC Q49LS1;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE XK-related protein 7.
GN Name=XKR7; Synonyms=XRG7;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pan.
OX NCBI_TaxID=9598;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Huang C.-H.; Chen Y.;
RT "A superfamily of XK-related genes (XRG) widely expressed in
RT vertebrates and invertebrates."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -!- SIMILARITY: Belongs to the XK family.
CC -----
CC Copyrighted under the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR ENBL; AV702910; AAV83783.1; -; mRNA.
KW Membrane; Transmembrane.
FT CHAIN 1 579 XK-related protein 7.
FT TRANSMEM 59 79 /FTId=PRO_0000190790.
FT TRANSMEM 89 109 Potential.
FT TRANSMEM 260 280 Potential.
FT TRANSMEM 314 334 Potential.
FT TRANSMEM 355 375 Potential.
FT TRANSMEM 384 404 Potential.
FT TRANSMEM 415 435 Potential.
SQ SEQUENCE 579 AA; 63593 MW; 6DFE1191093E85D4 CRC64;

Query Match 49.0%; Score 48; DB 1; Length 579;
Best Local Similarity 50.0%; Pred. No. 77;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSWRFIRAF 17
   :||:|
Db 190 LGQWRYLRALY 201

```

```

RT RT "A superfamily of XK-related genes (XRG) widely expressed in
RT vertebrates and invertebrates."
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -!- SIMILARITY: Belongs to the XK family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY534261; AAT07110.1; -; mRNA.
KW Membrane; Transmembrane.
CHAIN 1 580 XK-related protein 7.
FT TRANSMEM 59 79 Potential.
FT TRANSMEM 89 109 Potential.
FT TRANSMEM 260 280 Potential.
FT TRANSMEM 303 323 Potential.
FT TRANSMEM 326 346 Potential.
FT TRANSMEM 355 375 Potential.
FT TRANSMEM 384 404 Potential.
FT TRANSMEM 415 435 Potential.
SQ SEQUENCE 580 AA; 64338 MW; 8F4907F391B4F5BE CRC64;

Query Match 49.0%; Score 48; DB 1; Length 580;
Best Local Similarity 50.0%; Pred. No. 77;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 6 IGSWRFIRAFY 17
Db 190 LGQVWRYLRALY 201

RESULT 12
QSAUSS_EMENI PRELIMINARY; PRT; 597 AA..
AC QSAUSS;
DT 26-APR-2005, integrated into UniProtKB/TREMBL.
DT 26-APR-2005, sequence version 1.
DT 07-MAR-2006, entry version 6.
DE Hypothetical protein.
GN ORFNames=AN7955.2;
OS Aspergillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OC NCBI_TaxID=227321;
RN [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=FGSC 4;
RX PubMed=16372000; DOI=10.1038/nature04341;
RA Galagan J.E., Calvo S.E., Cuomo C., Ma L.-J., Wortman J.R.,
RA Batzoglou S., Lee S.-I., Bastuerkmen M., Spevak C.C., Clutterbuck J.,
RA Kapitonov V., Jurka J., Scaccocchio C., Farman M., Butler J.,
RA Purcell S., Harris S., Braus G.H., Drant O., Busch S., D'Enfert C.,
RA Bouchier C., Goldman G.H., Bell-Pedersen D., Griffiths-Jones S.,
RA Doonan J.H., Yu J., Vienken K., Pain A., Freitag M., Selker E.U.,
RA Archer D.B., Penalva M.A., Oakley B.R., Momany M., Tanaka T.,
RA Kumagai T., Asai K., Machida M., Nierman W.C., Denning D.W.,
RA Caddick M., Hynes M., Paoletti M., Fischer R., Miller B.L., Dyer P.S.,
RA Sachs M.S., Osmani S.A., Birren B.W.;
RA "Sequencing of Aspergillus nidulans and comparative analysis with A.
RT fumigatus and A. oryzae."
RL Nature 438:1105-1115 (2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AACD01000135; EAA59609.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015205; F:nucleobase transporter activity; IEA.

```

```

DR GO: GO:0015931; P:nucleobase, nucleoside, nucleotide and nucl. . . ; IEA.
DR InterPro; IPR001248; Cyt_pur_peroxidase.
DR Pfam; PF01333; Transp_cyt_pur; 1.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65089 MW; E686F4978F37BF5E CRC64;

Query Match 49.0%; Score 48; DB 2; Length 597;
Best Local Similarity 47.1%; Pred. No. 79;
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 LRRFIGSIWRFIRAFYG 18
||| . . . . .
Db 159 LRSFVGCMWFGMQAFWG 175

RESULT 13
P74489_SNNY3
ID P74489_SNNY3 PRELIMINARY; PRT; 627 AA.
AC P74489
DT 01-FEB-1997, integrated into UniProtKB/TrEMBL.
DT 01-FEB-1997, sequence version 1.
DT 07-FEB-2006, entry version 29.
DE S111858 protein.
GN OrderedLocustNames=s111858;
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=97061201; Pubmed=9905231; DOI=10.1093/dnares/3.3.109;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugiyura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RA "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RNA Res. 3:109-136(1996).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; BA000022; BA118591.1; -; Genomic_DNA.
DR PIR; S76462; S76462.
DR BioCyc; SSP1148:SLI1858-MONOMER; -.
KW Complete proteome.
SQ SEQUENCE 627 AA; 69725 MW; BBE187A53BF96229 CRC64;

Query Match 49.0%; Score 48; DB 2; Length 627;
Best Local Similarity 38.9%; Pred. No. 83;
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 GLRRFIGSIWRFIRAFYG 18
||| . . . . .
Db 597 GLEQLGKIWQLKQKEG 614

RESULT 14
Q44QDI_CHLLI
ID Q44QDI_CHLLI PRELIMINARY; PRT; 805 AA.
AC Q44QDI;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 21-FEB-2006, entry version 9.
DE Leucyl-tRNA synthetase bacterial/mitochondrial, class Ia.
GN ORPNames=ClinDRAFT_1980;
OS Chlorobium limicola DSM 245.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium/Pelodictyon group; Chlorobium.
OX NCBI_TaxID=290315;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```

```

RC STRAIN=DSM 245;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Chlorobium limicola
DSM 245.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 245;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Chlorobium limicola DSM
245.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AAHJ01000009; EAM43320.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
DR GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
DR InterPro; IPR002302; Leu_trna_sylt_1; 1.
DR Pfam; PF00133; tRNA-synt_1; 1.
DR PRINTS; PRO0985; TRNASYNTHLEU.
DR TIGRFAMS; TIGR00396; leuS_bact; 1.
KW Aminoacyl-tRNA synthetase.
SQ SEQUENCE 805 AA; 91997 MW; D4F3FE28F9E2DF3 CRC64;

Query Match 49.0%; Score 48; DB 2; Length 805;
Best Local Similarity 46.2%; Pred. No. 11e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLRRFIGSIWRFI 13
|: |: |: |: |:
Db 622 GTSRFLGKVRLLV 634

RESULT 15
Q43K01_9CHLB
ID Q43K01_9CHLB PRELIMINARY; PRT; 816 AA.
AC Q43K01;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 21-FEB-2006, entry version 9.
DE Leucyl-tRNA synthetase bacterial/mitochondrial, class Ia.
GN ORPNames=Cpha266DRAFT_2546;
OS Chlorobium phaeobacteroides DSM 266.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium/Pelodictyon group; Chlorobium.
OX NCBI_TaxID=290317;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 266;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome and assembly of Chlorobium
phaeobacteroides DSM 266.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 266;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Chlorobium
phaeobacteroides DSM 266.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an

```

```

CC      EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC      preliminary data.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonDerivs License
CC      -----
DR      EMBL; AAIB01000002; EAM35935.1; -; Genomic_DNA.
DR      GO; GO:0005524; P:ATP binding; IEA.
DR      GO; GO:0004823; P:leucine-tRNA ligase activity; IEA.
DR      GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
DR      InterPro; IPR002302; Leu_tRNAasn_1a.
DR      Pfam; PF00133; tRNA-synt_1; 1.
DR      PRINTS; PR00985; TRNASYNTHLEU.
DR      TIGRFAMs; TIGR00396; leus_bact; 1.
KW      Aminoacyl-tRNA synthetase_
SQ      SEQUENCE 816 AA; 93335 MW; 6770B1DAC50560F1 CRC64;

Query Match 49.0%; Score 48; DB 2; Length 816;
Best Local Similarity 46.2%; Pred. NO. 1.1e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy      1 GLRRFIGSIWRFI 13
Db      622 GISRFLGKVKVRLV 634

```

Search completed: May 19, 2006, 14:38:14
Job time : 115.429 secs

This Page Blank (uspto)

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRIFAFVG 18
|:::|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 2
US-08-940-093-242
; Sequence 242, Application US/08940093
; Patent No. 6037323
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Cornut, Isabelle
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,093
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6037323e
; US-08-940-093-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRIFAFVG 18
|:::|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 3
US-08-940-096-242
; Sequence 242, Application US/08940096
; Patent No. 6046166
; GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,096
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6046166e
; US-08-940-096-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRIFAFVG 18
|:::|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 4
US-09-465-719-242
; Sequence 242, Application US/09465719
; Patent No. 6265377
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/465,719
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,093
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6265377e
; US-09-465-719-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRFIKAFVG 18
|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 5
US-09-453-605-242
; Sequence 242, Application US/09453605
; Patent No. 6329341
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6376464e
; US-09-453-605-242
```

```
;
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6329341e
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:
; US-09-453-605-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRFIKAFVG 18
|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 6
US-09-453-838-242
; Sequence 242, Application US/09453838
; Patent No. 6376464
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,838
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6376464e
; US-09-453-838-242
```

```
US-09-453-838-242
Query Match          75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRFFIRAFVG 18
|:::|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 7
US-08-940-136-242
; Sequence 242, Application US/08940136
; Patent No. 6518412
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Metz, Isabelle
; APPLICANT: Cornut, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,136
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0007-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6518412e
US-08-940-136-242

Query Match          75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRFFIRAFVG 18
|:::|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 8
US-09-453-841-242
; Sequence 242, Application US/09453841
; Patent No. 6573239
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Metz, Isabelle
; APPLICANT: Cornut, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,841
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6573239e
US-09-453-841-242

Query Match          75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRFFIRAFVG 18
|:::|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 9
US-09-453-833-242
; Sequence 242, Application US/09453833
; Patent No. 6602854
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Metz, Isabelle
; APPLICANT: Cornut, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
```

```
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,833
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6602854e
; US-09-453-833-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRFIRAFYG 18
|:::|||||:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 10
US-09-453-826-242
; Sequence 242, Application US/09453826
; Patent No. 6630450
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,826
; FILING DATE:
; CLASSIFICATION:
```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6630450e
; US-09-453-826-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRFIRAFYG 18
|:::|||||:|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 11
US-09-453-840-242
; Sequence 242, Application US/09453840
; Patent No. 6716816
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,840
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
```

```
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6716816e
US-09-453-840-242
Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRFIRAFYG 18
|:::|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 12
US-09-865-989-242
; Sequence 242, Application US/09865989
; Patent No. 6734169
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,989
; FILING DATE: 25-May-2001
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/465,719
; FILING DATE: 17-DEC-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6734169e
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-865-989-242
Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRFIRAFYG 18
|:::|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 13
US-09-453-834-242
; Sequence 242, Application US/09453834
; Patent No. 6753313
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,834
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6753313e
; US-09-453-834-242
Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRFIRAFYG 18
|:::|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 14
US-10-283-599-242
; Sequence 242, Application US/10283599
; Patent No. 6844327
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
```

TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.

NUMBER OF SEQUENCES: 274

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/283,599

FILING DATE: 29-OCT-2002

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/940,136

FILING DATE: 29-SEP-1997

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009196-0007-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 242:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6844327e

US-10-283-599-242

Query Match 75.5%; Score 74; DB 2; Length 18;

Best Local Similarity 61.1%; Pred. No. 3.9e-05;

Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRPIRAFYG 18

Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 15

US-09-465-718-242

Sequence 242, Application US/09465718

Patent No. 6900177

GENERAL INFORMATION:

APPLICANT: Dasseux, Jean-Louis

APPLICANT: Sekul, Renate

APPLICANT: Buttner, Klaus

APPLICANT: Cornut, Isabelle

APPLICANT: Metz, Gunther

TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

NUMBER OF SEQUENCES: 258

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/465,718

FILING DATE: 17-Dec-1999

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/940,096

FILING DATE: 29-SEP-1997

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 009196-0005-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 242:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: No. 6900177e

US-09-465-718-242

Query Match 75.5%; Score 74; DB 2; Length 18;

Best Local Similarity 61.1%; Pred. No. 3.9e-05;

Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRPIRAFYG 18

Db 1 GIKKFLGSIWKFIKAFVG 18

Search completed: May 19, 2006, 14:42:55

Job time : 24.8571 secs

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 15:18:19 ; Search time 81.2857 seconds
(without alignments)

102.575 Million cell updates/sec

Title: US-10-712-447-115

Perfect score: 98

Sequence: 1 GLRRFGSIWRIFAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US07_PUBCOMB.psp.*
- 2: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US08_PUBCOMB.psp.*
- 3: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US09_PUBCOMB.psp.*
- 4: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US10A_PUBCOMB.psp.*
- 5: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US10B_PUBCOMB.psp.*
- 6: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US11_PUBCOMB.psp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	18	4	US-10-712-447-115
2	98	100.0	18	4	US-10-712-447-116
3	94	95.9	18	4	US-10-712-447-2
4	94	95.9	18	4	US-10-712-447-5
5	94	95.9	18	4	US-10-712-447-8
6	94	95.9	18	4	US-10-712-447-10
7	94	95.9	18	4	US-10-712-447-13
8	94	95.9	18	4	US-10-712-447-117
9	94	95.9	18	4	US-10-712-447-127
10	94	95.9	18	4	US-10-712-447-131
11	91	92.9	18	4	US-10-712-447-91
12	90	91.8	18	4	US-10-712-447-129
13	88	89.8	18	4	US-10-712-447-21
14	88	89.8	18	4	US-10-712-447-53
15	88	89.8	18	4	US-10-712-447-74
16	86	87.8	18	4	US-10-712-447-4
17	86	87.8	18	4	US-10-712-447-112
18	85	86.7	18	4	US-10-712-447-99
19	84	85.7	18	4	US-10-712-447-18
20	84	85.7	18	4	US-10-712-447-113
21	84	85.7	18	4	US-10-712-447-114
22	83	84.7	18	4	US-10-712-447-17
23	83	84.7	18	4	US-10-712-447-121
24	82	83.7	18	4	US-10-712-447-61
25	82	83.7	18	4	US-10-712-447-82
26	81	82.7	18	4	US-10-712-447-16
27	81	82.7	18	4	US-10-712-447-96

Sequence 22, Appl
Sequence 78, Appl
Sequence 95, Appl
Sequence 120, Appl
Sequence 19, Appl
Sequence 56, Appl
Sequence 58, Appl
Sequence 77, Appl
Sequence 80, Appl
Sequence 94, Appl
Sequence 97, Appl
Sequence 119, Appl
Sequence 242, Appl
Sequence 242, Appl

ALIGNMENTS

RESULT 1

US-10-712-447-115

; Sequence 115, Application US/10712447

; Publication No. US20040186057A1

; GENERAL INFORMATION:

; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

; APPLICANT: GARBBER, DAVID W.

; APPLICANT: DATTA, GEETA

; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

; FILE REFERENCE: 112739-123US

; CURRENT APPLICATION NUMBER: US/10/712,447

; CURRENT FILING DATE: 2003-11-13

; PRIOR APPLICATION NUMBER: 60/425,821

; PRIOR FILING DATE: 2002-11-13

; NUMBER OF SEQ ID NOS: 210

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 115

; LENGTH: 18

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: peptide

US-10-712-447-115

Query Match 100.0%; Score 98; DB 4; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.2e-07;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRIFAFYG 18

Db 1 GLRRFGSIWRIFAFYG 18

RESULT 2

US-10-712-447-116

; Sequence 116, Application US/10712447

; Publication No. US20040186057A1

; GENERAL INFORMATION:

; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.

; APPLICANT: GARBBER, DAVID W.

; APPLICANT: DATTA, GEETA

; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING

; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE

; FILE REFERENCE: 112739-123US

; CURRENT APPLICATION NUMBER: US/10/712,447

; CURRENT FILING DATE: 2003-11-13

; PRIOR APPLICATION NUMBER: 60/425,821

; PRIOR FILING DATE: 2002-11-13

```
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 116
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; US-10-712-447-116

Query Match          100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRFIRAFYG 18
   |:|:|:|:|:|:|:|:|:|:|
Db 1 GLRRFGSIWRFIRAFYG 18

RESULT 3
US-10-712-447-2
; Sequence 2, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; OTHER INFORMATION: c-term amidated
; US-10-712-447-2

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRFIRAFYG 18
   |:|:|:|:|:|:|:|:|:|:|
Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 4
US-10-712-447-5
; Sequence 5, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 10
; LENGTH: 18

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRFIRAFYG 18
   |:|:|:|:|:|:~|:|:|:|:|
Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 5
US-10-712-447-8
; Sequence 8, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; US-10-712-447-8

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRFIRAFYG 18
   |:|:|:~|:|:|:|:|:|:|:|
Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 6
US-10-712-447-10
; Sequence 10, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 10
; LENGTH: 18
```


This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 15:18:37 ; Search time 2.14286 Seconds
(without alignments)
17.943 Million cell updates/sec

Title: US-10-712-447-115

Perfect score: 98

Sequence: 1 GLRRFIGSIWRPAPVY 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pap.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pap.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pap.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pap.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pap.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pap.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pap.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	38.8	74	1	US-09-949-925-111
2	37.5	38.3	441	6	US-10-511-937-2947
3	35	35.7	651	6	US-10-511-937-2401
4	34.5	35.2	60	1	US-09-949-925-142
5	34	34.7	522	6	US-10-505-928-543
6	34	34.7	599	7	US-11-302-678-5
7	33.5	34.2	244	7	US-11-169-140-109
8	33.5	34.2	503	7	US-11-024-544A-21
9	33.5	34.2	503	7	US-11-190-750-135
10	33.5	34.2	503	7	US-11-264-784-87
11	33	33.7	313	7	US-11-242-505A-48
12	33	33.7	342	7	US-11-204-427-7
13	33	33.7	393	7	US-11-304-129-40
14	33	33.7	393	7	US-11-304-129-48
15	33	33.7	403	7	US-11-242-505A-18
16	33	33.7	463	6	US-10-505-928-545
17	33	33.7	643	6	US-10-504-120-19
18	33	33.7	667	7	US-11-311-555-16
19	33	33.7	677	6	US-11-311-561-16
20	33	33.7	714	6	US-10-868-498-2
21	33	33.7	919	7	US-11-302-678-62
22	32	32.7	351	6	US-10-511-937-2540
23	32	32.7	364	7	US-11-113-081A-6
24	32	32.7	388	6	US-10-196-749-336
25	32	32.7	388	7	US-11-024-544A-169

Sequence 137, App
Sequence 1, Appli
Sequence 12, Appl
Sequence 17, Appl
Sequence 859, App
Sequence 88, Appl
Sequence 2, Appli
Sequence 6, Appli
Sequence 569, App
Sequence 23, Appl
Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 23, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 26, Appl
Sequence 6, Appli
Sequence 18, Appl
Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-949-925-111
; Sequence 111, Application US/09949925
; Publication No. US2006009575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (74)
; OTHER INFORMATION: Xaa equals stop translation
US-09-949-925-111

Query Match 38.8%; Score 38; DB 1; Length 74;
Best Local Similarity 63.6%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 LRRFIGSIWRP 12
||| |

; PRIOR APPLICATION NUMBER: US 60/363,019
 ; PRIOR FILING DATE: 2002-03-07
 ; NUMBER OF SEQ ID NOS: 866
 ; SOFTWARE: PatentIn 3.2
 ; SEQ ID NO 543
 ; LENGTH: 522
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-505-928-543

Query Match 34.7%; Score 34; DB 6; Length 522;
 Best Local Similarity 47.1%; Pred. No. 55;
 Matches 8; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 3 RRFI--GSIWRFIRAFY 17
 ||| :|:|:|:|
 Db 473 RRFQSGDLYHRKRFH 489

RESULT 6
 US-11-302-678-5
 ; Sequence 5, Application US/11302678
 ; Publication No. US2006008881A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Silos-Santiago, Inmaculada
 ; APPLICANT: Venkateswarlu, Karicheti
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
 ; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
 ; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
 ; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
 ; FILE REFERENCE: MPI02-012P1RM OMNI
 ; CURRENT APPLICATION NUMBER: US/11/302,678
 ; CURRENT FILING DATE: 2005-12-14
 ; PRIOR APPLICATION NUMBER: US/10/345,680
 ; PRIOR FILING DATE: 2003-01-16
 ; PRIOR APPLICATION NUMBER: US 60/349,511
 ; PRIOR FILING DATE: 2002-01-18
 ; PRIOR APPLICATION NUMBER: US 60/360,500
 ; PRIOR FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 60/365,041
 ; PRIOR FILING DATE: 2002-03-15
 ; PRIOR APPLICATION NUMBER: US 60/374,063
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: US 60/403,468
 ; PRIOR FILING DATE: 2002-08-14
 ; PRIOR APPLICATION NUMBER: US 60/414,262
 ; PRIOR FILING DATE: 2002-09-27
 ; PRIOR APPLICATION NUMBER: US 60/419,986
 ; PRIOR FILING DATE: 2002-10-21
 ; PRIOR APPLICATION NUMBER: US 60/423,809
 ; PRIOR FILING DATE: 2002-11-05
 ; PRIOR APPLICATION NUMBER: US 60/429,797
 ; PRIOR FILING DATE: 2002-11-26
 ; NUMBER OF SEQ ID NOS: 66
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 599
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; US-11-302-678-5

Query Match 34.7%; Score 34; DB 7; Length 599;
 Best Local Similarity 57.1%; Pred. No. 64;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 6 IGSIWRF 12
 :|:|:|:|
 Db 64 LGVWRF 70

RESULT 7
 US-11-169-140-109

; Sequence 109, Application US/11169140
 ; Publication No. US20060099150A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
 ; APPLICANT: HOUSTON, Lou, L.
 ; APPLICANT: SHERIDAN, Philip, J.
 ; APPLICANT: HAWLEY, Stephen
 ; APPLICANT: GLYNN, Jacqueline, M.
 ; APPLICANT: CHAPIN, Steven
 ; TITLE OF INVENTION: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CEI
 ; TITLE OF INVENTION: BARRIERS
 ; FILE REFERENCE: 11474-037-999
 ; CURRENT APPLICATION NUMBER: US/11/169,140
 ; CURRENT FILING DATE: 2005-06-27
 ; PRIOR APPLICATION NUMBER: US 60/267,601
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: US 60/248,819
 ; PRIOR FILING DATE: 2000-11-14
 ; PRIOR APPLICATION NUMBER: US 60/248,478
 ; PRIOR FILING DATE: 2000-11-13
 ; PRIOR APPLICATION NUMBER: US 60/237,929
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: 09/949,039
 ; PRIOR FILING DATE: 2001-09-06
 ; PRIOR APPLICATION NUMBER: 09/969,748
 ; PRIOR FILING DATE: 2001-10-02
 ; NUMBER OF SEQ ID NOS: 143
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 109
 ; LENGTH: 244
 ; TYPE: PRT
 ; ORGANISM: Simian
 ; US-11-169-140-109

Query Match 34.2%; Score 33.5; DB 7; Length 244;
 Best Local Similarity 42.1%; Pred. No. 27;
 Matches 8; Conservative 3; Mismatches 3; Indels 5; Gaps 1;

Qy 1 GLRRFIGSIW-----RFR 14
 || :|:|:|:|
 Db 158 GLVLALGAVMVARAFIR 176

RESULT 8
 US-11-024-544A-21
 ; Sequence 21, Application US/11024544A
 ; Publication No. US20060094086A1
 ; GENERAL INFORMATION:
 ; APPLICANT: E.I. duPont de Nemours and Company, Inc.
 ; APPLICANT: Yadav, Narendra
 ; APPLICANT: Xue, Zhixiong
 ; APPLICANT: Zhang, Hongxiang
 ; TITLE OF INVENTION: DIACYLGLYCEROL ACYLTRANSFERASES FOR ALTERATION OF POLYUNSATURATED
 ; FILE REFERENCE: CL2717
 ; CURRENT APPLICATION NUMBER: US/11/024,544A
 ; CURRENT FILING DATE: 2004-12-29
 ; NUMBER OF SEQ ID NOS: 175
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 21
 ; LENGTH: 503
 ; TYPE: PRT
 ; ORGANISM: Magnaporthe grisea 70-15
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: GenBank Accession No. EAA52634
 ; DATABASE ENTRY DATE: 2003-10-31
 ; RELEVANT RESIDUES: (1)..(503)
 ; US-11-024-544A-21

Query Match 34.2%; Score 33.5; DB 7; Length 503;
 Best Local Similarity 43.8%; Pred. No. 64;
 Matches 7; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 3 RRFISWRFIRAFY 18
|||: ||: | : |
Db 156 RRFV-STWKLIALVHG 170

RESULT 9
US-11-190-750-135
; Sequence 135, Application US/11190750
; Publication No. US20060094089A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Yadav, Narendra
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS TO INCREASE THE PERCENT OF
; TITLE OF INVENTION: ACYTRANSFERRASE REGULATION TO INCREASE THE PERCENT OF
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN TOTAL LIPIDS AND OILS OF
; FILE REFERENCE: CL2718
; CURRENT APPLICATION NUMBER: US/11/190,750
; CURRENT FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 135
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Magnaporthe grisea 70-15 [GenBank Accession No. EAA52634]
US-11-190-750-135

Query Match 34.2%; Score 33.5; DB 7; Length 503;
Best Local Similarity 43.8%; Pred. No. 64;
Matches 7; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 3 RRFISWRFIRAFY 18
|||: ||: | : |
Db 156 RRFV-STWKLIALVHG 170

RESULT 10
US-11-264-784-87
; Sequence 87, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 87
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Magnaporthe grisea 70-15 [GenBank Accession No. EAA52634]
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: DGAT1
US-11-264-784-87

Query Match 34.2%; Score 33.5; DB 7; Length 503;
Best Local Similarity 43.8%; Pred. No. 64;
Matches 7; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 3 RRFISWRFIRAFY 18

Db 156 RRFV-STWKLIALVHG 170
|||: ||: | : |

RESULT 11
US-11-242-505A-48
; Sequence 48, Application US/11242505A
; Publication No. US2006009956A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310, c
; FILE REFERENCE: MPI2001-288P1RCPIONNIM
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-242-505A-48

Query Match 33.7%; Score 33; DB 7; Length 313;
Best Local Similarity 62.5%; Pred. No. 45;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 WRFIRAFY 17
||: ||: ||
Db 199 WSFLDAFY 206

RESULT 12
US-11-204-427-7
; Sequence 7, Application US/11204427
; Publication No. US20060100146A1
; GENERAL INFORMATION:
; APPLICANT: Turley, Stephen L
; APPLICANT: Turkish, Aaron R
; APPLICANT: Billheimer, Jeffrey T
; APPLICANT: Cromley, Debra
; TITLE OF INVENTION: AWAT-RELATED METHODS AND ARTICLES
; FILE REFERENCE: 0575/72796/JPW/AJM/JCS
; CURRENT APPLICATION NUMBER: US/11/204,427
; CURRENT FILING DATE: 2005-08-15
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-204-427-7

Query Match 33.7%; Score 33; DB 7; Length 342;
Best Local Similarity 50.0%; Pred. No. 50;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 8 SIWRFIRAFY 17
: ||: ||: ||
Db 84 AIWQRDRYY 93

RESULT 13

US-11-304-129-40
; Sequence 40, Application US/11304129
; Publication No. US20060088915A1
; GENERAL INFORMATION:
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: TAKATSU, Yoshihiro
; APPLICANT: WATANABE, Takuya
; APPLICANT: TERAU, Yasuko
; APPLICANT: SHINTANI, Yasushi
; APPLICANT: HINUMA, Syuji
; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
; FILE REFERENCE: 2762USOP
; CURRENT APPLICATION NUMBER: US/11/304,129
; CURRENT FILING DATE: 2005-12-15
; PRIOR APPLICATION NUMBER: US/10/333,192
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: JP 2000-217442
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: JP 2001-26779
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/JP01/06162
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 40
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Rat
US-11-304-129-40

Query Match 33.7%; Score 33; DB 7; Length 393;
Best Local Similarity 46.2%; Pred. No. 58;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 FIGSIWRFIRAFY 17
Db 216 FCGIWPVDQFY 228

RESULT 14
US-11-304-129-48
; Sequence 48, Application US/11304129
; Publication No. US20060088915A1
; GENERAL INFORMATION:
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: TAKATSU, Yoshihiro
; APPLICANT: WATANABE, Takuya
; APPLICANT: TERAU, Yasuko
; APPLICANT: SHINTANI, Yasushi
; APPLICANT: HINUMA, Syuji
; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
; FILE REFERENCE: 2762USOP
; CURRENT APPLICATION NUMBER: US/11/304,129
; CURRENT FILING DATE: 2005-12-15
; PRIOR APPLICATION NUMBER: US/10/333,192
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: JP 2000-217442
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: JP 2001-26779
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/JP01/06162
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 58
; SEQ ID NO 48
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Mouse
US-11-304-129-48

Query Match 33.7%; Score 33; DB 7; Length 393;
Best Local Similarity 46.2%; Pred. No. 58;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 FIGSIWRFIRAFY 17
Db 216 FCGIWPVDQFY 228

RESULT 15
US-11-242-505A-18
; Sequence 18, Application US/11242505A
; Publication No. US20060099656A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
; FILE REFERENCE: MPI2001-288P1RCP1OWNIM
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-242-505A-18

Query Match 33.7%; Score 33; DB 7; Length 403;
Best Local Similarity 44.4%; Pred. No. 60;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LRRFIGSIW 10
Db 155 VRRVIGAVW 163

Search completed: May 19, 2006, 15:28:18
Job time : 2.14286 secs

This Page Blank (uspio)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocollaboration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:13:22 ; Search time 94.2857 seconds
(without alignments)

87.287 Million cell updates/sec

Title: US-10-712-447-116

Perfect score: 98

Sequence: 1 GLRRFGSIWRFIRAFYK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq 8:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

9: Geneseqp2005s:*

10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	18	ADO34338	Synthetic
2	98	100.0	18	ADO34339	Synthetic
3	94	95.9	18	ADO34231	Synthetic
4	94	95.9	18	ADO34354	Synthetic
5	94	95.9	18	ADO34225	Synthetic
6	94	95.9	18	ADO34228	Synthetic
7	94	95.9	18	ADO34236	Synthetic
8	94	95.9	18	ADO34340	Synthetic
9	94	95.9	18	ADO34233	Synthetic
10	94	95.9	18	ADO34350	Synthetic
11	91	92.9	18	ADO34314	Synthetic
12	90	91.8	18	ADO34352	Synthetic
13	88	89.8	18	ADO34297	Synthetic
14	88	89.8	18	ADO34244	Synthetic
15	88	89.8	18	ADO34276	Synthetic
16	86	87.8	18	ADO34227	Synthetic
17	86	87.8	18	ADO34335	Synthetic
18	85	86.7	18	ADO34322	Synthetic
19	84	85.7	18	ADO34336	Synthetic
20	84	85.7	18	ADO34337	Synthetic
21	84	85.7	18	ADO34241	Synthetic
22	83	84.7	18	ADO34240	Synthetic
23	83	84.7	18	ADO34344	Synthetic

24	82	83.7	18	8	ADO34284	Synthetic
25	82	83.7	18	8	ADO34305	Synthetic
26	81	82.7	18	8	ADO34239	Synthetic
27	81	82.7	18	8	ADO34319	Synthetic
28	80	81.6	18	8	ADO34245	Synthetic
29	80	81.6	18	8	ADO34301	Synthetic
30	80	81.6	18	8	ADO34343	Synthetic
31	80	81.6	18	8	ADO34318	Synthetic
32	78	79.6	18	8	ADO34302	Synthetic
33	78	79.6	18	8	ADO34279	Synthetic
34	78	79.6	18	8	ADO34303	Synthetic
35	78	79.6	18	8	ADO34242	Synthetic
36	78	79.6	18	8	ADO34300	Synthetic
37	78	79.6	18	8	ADO34281	Synthetic
38	78	79.6	18	8	ADO34317	Synthetic
39	77	78.6	18	8	ADO34323	Synthetic
40	77	78.6	18	8	ADO34280	Synthetic
41	76	77.6	18	8	ADO34264	Synthetic
42	76	77.6	18	8	ADO34342	Synthetic
43	75	76.5	18	8	ADO34320	Synthetic
44	74	75.5	18	2	AA118917	Lecithin:
45	74	75.5	18	2	AA119171	Lecithin:

ALIGNMENTS

RESULT 1

ID ADO34338 standard; peptide; 18 AA.

AC ADO34338;

DT 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 115.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;
KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
XX low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

PN 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 115; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
CC polypeptide. The invention further comprises an isolated nucleic acid
CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
CC a host cell, a recombinant cell or a transgenic, non-human subject
CC (including animal or plant) comprising the synthetic apolipoprotein-E
CC mimicking polypeptide encoding polynucleotide; a composition comprising
CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
CC an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipemic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 XX Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5.2e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRRFIGSIWRFIRAFYG 18
 |||||
 Db 1 GLRRFIGSIWRFIRAFYG 18

RESULT 2

ADO34339
 ID ADO34339 standard; peptide; 18 AA.

AC ADO34339;

XX 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 116.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 116; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipemic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5.2e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRRFIGSIWRFIRAFYG 18
 |||||
 Db 1 GLRRFIGSIWRFIRAFYG 18

RESULT 3

ADO34231

ID ADO34231 standard; peptide; 18 AA.

AC ADO34231;

XX 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 8.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 8; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipemic,

CC cardiatic, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.1e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRRFIGSIWRIFAFYVG 18
 |.|||.|||||.|||||
 Db 1 GIRFLGSIWRIFAFYVG 18

RESULT 4
 ADO34354
 ID ADO34354 standard; peptide, 18 AA.

XX
 AC ADO34354;

XX
 DT 12-AUG-2004 (first entry)

XX
 DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 131.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiac;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX
 OS Synthetic.

XX
 PN WO2004043403-A2.

XX
 PD 27-MAY-2004.

XX
 PF 13-NOV-2003; 2003WO-US036268.

XX
 PR 13-NOV-2002; 2002US-0425821P.

XX
 PA (UABR-) UAB RES FOUND.

XX
 PI Anantharamiah GM, Garber DW, Datta G;

XX
 DR WPI; 2004-411629/38.

XX
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX
 PS Claim 4; SEQ ID NO 131; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipemic,
 CC cardiac, vasotropic, antiarteriosclerotic, cerebroprotective, and

CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.1e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRRFIGSIWRIFAFYVG 18
 |.|||.|||||.|||||
 Db 1 GLRRFLGSIWRIFAFYVG 18

RESULT 5
 ADO34225
 ID ADO34225 standard; peptide, 18 AA.

XX
 AC ADO34225;

XX
 DT 12-AUG-2004 (first entry)

XX
 DE Synthetic apolipoprotein-E mimicking polypeptide related R18L peptide.

XX apolipoprotein-E mimicking polypeptide; antilipemic; cardiac;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX
 OS Synthetic.

XX
 Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 18

FT /note= "C-terminal amide"

XX
 PN WO2004043403-A2.

XX
 PD 27-MAY-2004.

XX
 PF 13-NOV-2003; 2003WO-US036268.

XX
 PR 13-NOV-2002; 2002US-0425821P.

XX
 PA (UABR-) UAB RES FOUND.

XX
 PI Anantharamiah GM, Garber DW, Datta G;

XX
 DR WPI; 2004-411629/38.

XX
 PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX
 PS Claim 4; SEQ ID NO 2; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.1e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRFIRAFVG 18
 |:|||||:|||||
 Db 1 GIRRFLGSIWRFIRAFVG 18

RESULT 8

ADO34340
 ID ADO34340 standard; peptide; 18 AA.

XX AC ADO34340;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 117.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 117; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 2.1e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRFIRAFVG 18
 |:|||||:|||||
 Db 1 GIRRFLGSIWRFIRAFVG 18

RESULT 9

ADO34233
 ID ADO34233 standard; peptide; 18 AA.

XX AC ADO34233;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 10.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 10; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,

polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is useful for reducing serum cholesterol in a subject (including a mammal such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,

The invention relates to a novel synthetic apolipoprotein-E mimicking polypeptide. The invention further comprises an isolated nucleic acid encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector, a host cell, a recombinant cell or a transgenic, non-human subject (including animal or plant) comprising the synthetic apolipoprotein-E mimicking polypeptide encoding polynucleotide; a composition comprising the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and an monoclonal antibody that specifically binds to the synthetic apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E mimicking polypeptide has the following activities: antilipemic, cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

CC useful for reducing serum cholesterol in a subject (including a mammal
CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
CC chimpanzee or orangutan); for treating coronary artery disease,
CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
CC myocardial infarction or stroke; for breaking an embolus in the subject;
CC and also for treating angina. The synthetic apolipoprotein-E mimicking
CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
CC mimicking polypeptide of the invention.

XX

SQ Sequence 18 AA;

Query Match 89.8%; Score 88; DB 8; Length 18;
Best Local Similarity 77.8%; Pred No. 1.8e-06;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRFIKAFYG 18

||:|||||:||||

Db 1 GIKRFLGSIWRFIKAFYG 18

Search completed: May 19, 2006, 14:24:31
Job time : 95.2857 secs

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:24:57 ; Search time 14.2857 Seconds
(without alignments)
121.233 Million cell updates/sec

Title: US-10-712-447-116
Perfect score: 98
Sequence: 1 GLRRFIGSIWRFIRAFYQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	48	49.0	627	2 S76462	hypothetical prote
2	47	48.0	516	2 T33269	hypothetical prote
3	45	45.9	489	2 B84733	probable cytochrom
4	44	44.9	246	2 I54412	MHC HLA-A cell sur
5	44	44.9	273	1 HLHU69	MHC class I histoc
6	44	44.9	365	1 HLHUA2	MHC class I histoc
7	44	44.9	365	2 I38443	Gene HLA-A-0203 pr
8	44	44.9	365	2 I61902	MHC class I histoc
9	44	44.9	365	2 I37542	MHC class I histoc
10	44	44.9	365	2 I84448	MHC class I histoc
11	44	44.9	365	2 I61857	MHC HLA-A2.4a chai
12	44	44.9	365	2 I38442	Gene HLA-A-0205 pr
13	44	44.9	589	2 A34341	poly(3-hydroxybuty
14	43	43.9	503	2 B81690	probable sodium-tr
15	43	43.9	519	1 T02263	cytochrome P450 DW
16	42.5	43.4	760	2 E84953	penicillin-binding
17	42	42.9	139	2 G64032	hypothetical prote
18	42	42.9	214	2 B72540	hypothetical prote
19	42	42.9	237	2 B72692	hypothetical prote
20	42	42.9	537	2 T04745	hypothetical prote
21	42	42.9	785	2 S63652	hypothetical prote
22	42	42.9	806	2 A84060	leucyl-tRNA synthet
23	42	42.9	861	2 H64102	leucine-tRNA ligas
24	42	42.9	1112	2 T42383	probable calcium-a
25	41.5	42.3	1025	2 A83568	acridin resista
26	41	41.8	178	2 A75578	transcription regu
27	41	41.8	265	2 T32316	hypothetical prote
28	41	41.8	265	2 C42595	rfaP protein - Bac
29	41	41.8	359	2 T20575	hypothetical prote

ALIGNMENTS

RESULT 1

S76462
hypothetical protein - Synecocystis sp. (strain PCC 6803)

C:Species: Synecocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: S76462

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis
s.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S76462

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-627 <KAN>

A:Cross-references: UNIPROT:P74489; UNIPARC:UPI000000C103F; EMBL:D90915; GB:AB001339; NID:
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 49.0%; Score 48; DB 2; Length 627;
Best Local Similarity 38.9%; Pred. No. 8.2; Indels 0; Gaps 0;
Matches 7; Conservative 6; Mismatches 5

Qy 1 GLRRFIGSIWRFIRAFYQ 18

Db 597 GLEQLLQKIQWLQKFG 614

RESULT 2

T33269
hypothetical protein C24B9.13 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C:Accession: T33269

R:Murray, J.; Wohldmann, P.; Langston, Y.; O'Neal, D.

submitted to the EMBL Data Library, May 1998

A:Description: The sequence of C. elegans cosmid C24B9.

A:Reference number: Z21310

A:Accession: T33269

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-516 <MUR>

A:Cross-references: UNIPROT:O76442; UNIPARC:UPI000000D477; EMBL:AF068709; PIDN:AAC19257.1

A:Experimental source: strain Bristol N2; clone C24B9

C:Genetics:

A:Gene: CESP:C24B9.13

A:Map position: 5

A:Introns: 13/3; 67/2; 116/2; 268/2; 315/2; 364/2

Query Match 48.0%; Score 47; DB 2; Length 516;
Best Local Similarity 52.9%; Pred. No. 9.8;

```

Matches      9;  Conservative      3;  Mismatches      5;  Indels      0;  Gaps      0;

Qy      2  LRRFIGSIWRFIRAFYG 18
      :|||:|:|:|:|:|:|
Db      252  LKPFITSLMFMHAFDG 268

RESULT 3
B84733
A;Title: Probable cytochrome P450 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: B84733
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shen, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B84733
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-489 <STO>
A;Cross-references: UNIPROT:Q9ZV72; UNIPARC:UPI000009D8ED; GB:AE002093; NID:g3831452; PI
C;Genetics:
A;Gene: At2g32440
A;Map position: 2
C;Superfamily: Synchocystis cytochrome P450 slr0574; cytochrome P450 homology

Query Match      45.9%; Score 45; DB 2; Length 489;
Best Local Similarity 63.6%; Pred. No. 19;
Matches      7;  Conservative      3;  Mismatches      1;  Indels      0;  Gaps      0;

Qy      6  IGSIWRFIRAF 16
      :|||:|:|:|:|:|
Db      54  IGNNWSFLRAF 64

RESULT 4
I54412
MHC HLA-A cell surface antigen - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: I54412
R;Arnot, D.; Lillie, J.W.; Auffray, C.; Kappes, D.; Strominger, J.L.
Immunogenetics 20, 237-252, 1984
A;Title: Inter-locus and intra-allelic polymorphisms of HLA class I antigen gene mRNA.
A;Reference number: I54412; MUID:84287690; PMID:6332068
A;Accession: I54412
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-246 <RES>
A;Cross-references: UNIPROT:Q29945; UNIPARC:UPI000008A27D; GB:M27537; NID:g187727; PIDN:
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: surface antigen
F;101-166/Domain: immunoglobulin homology <IMM>

Query Match      44.9%; Score 44; DB 2; Length 246;
Best Local Similarity 50.0%; Pred. No. 14;
Matches      6;  Conservative      4;  Mismatches      2;  Indels      0;  Gaps      0;

Qy      6  IGSIWRFIRAFY 17
      :|||:|:|:|:|:|
Db      8  VGSDWRFELRGYH 19

RESULT 5
HLHUG9
MHC class I histocompatibility antigen HLA-Aw69 alpha chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: B24671
R;Holmes, N.; Parham, P.

```

```

EMBO J. 4, 2849-2854, 1985
A;Title: Exon shuffling in vivo can generate novel HLA class I molecules.
A;Reference number: A91021; MUID:86055720; PMID:3877632
A;Accession: B24671
A;Molecule type: DNA
A;Residues: 1-273 <HOL>
A;Cross-references: UNIPROT:PI0316; UNIPARC:UPI0000124E4B
C;Genetics:
A;Gene: GDB:HLA-A
A;Cross-references: GDB:119310; OMIM:142800
A;Map position: 6p21.3-6p21.3
A;Superfamily: 89/3
C;Keywords: class I histocompatibility antigen; immunoglobulin homology
F;195-260/Domain: immunoglobulin homology <IMM>
F;85/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      44.9%; Score 44; DB 1; Length 273;
Best Local Similarity 50.0%; Pred. No. 16;
Matches      6;  Conservative      4;  Mismatches      2;  Indels      0;  Gaps      0;

Qy      6  IGSIWRFIRAFY 17
      :|||:|:|:|:|:|
Db      102  VGSDWRFELRGYH 113

RESULT 6
HLHUA2
MHC class I histocompatibility antigen HLA-A2 alpha chain precursor [validated] - human
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1980 #sequence_revision 22-Apr-1995 #text_change 08-Dec-2000
C;Accession: I55948; E35997; A02191; S19020; S77965; S23593; A93834; A93919; S14802; A021
R;Koller, B.H.; Orr, H.T.
J. Immunol. 134, 2727-2733, 1985
A;Title: Cloning and complete sequence of an HLA-A2 gene: Analysis of two HLA-A alleles
A;Reference number: I55948; MUID:85132727; PMID:2982951
A;Accession: I55948
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-365 <KOL>
A;Cross-references: UNIPARC:UPI0000124E24; GB:K02883; NID:g187605; PIDN:AAA98727.1; PID:
A;Experimental source: lymphoblastoid cell line 721
R;Ennis, P.D.; Zemmour, J.; Salter, R.D.; Parham, P.
Proc. Natl. Acad. Sci. U.S.A. 87, 2833-2837, 1990
A;Title: Rapid cloning of HLA-A,B cDNA by using the polymerase chain reaction: frequency
A;Reference number: A35997; MUID:90207291; PMID:2320591
A;Accession: E35997
A;Molecule type: mRNA
A;Residues: 1-365 <ENN>
A;Cross-references: UNIPARC:UPI0000124E24; GB:M84379; GB:M32322; NID:g403143; PIDN:AAA59
A;Note: this allele is designated A*0201 (previously HLA-A2.1)
R;Kragel, M.S.
EMBO J. 4, 1205-1210, 1985
A;Title: Unusual RNA splicing generates a secreted form of HLA-A2 in a mutagenized B lymph
A;Reference number: A02191; MUID:85230571; PMID:3874058
A;Accession: A02191
A;Molecule type: mRNA
A;Residues: 39-365 <KRA>
A;Cross-references: UNIPARC:UPI000016AA56; GB:X02457; NID:g32153; PIDN:CAA26297.1; PID:g:
A;Note: the author translated the codon CAG for residue 96 as His, ACU for residue 97 as
s Thr, and ACU for residue 323 as Ser
R;Castano, A.R.; Lopez de Castro, J.A.
Immunogenetics 34, 281-285, 1991
A;Title: Structure of the HLA-A*0204 antigen, found in South American Indians. Spatial cl
A;Reference number: S19020; MUID:92039809; PMID:1937577
A;Accession: S19020
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 9-120, M', 122-365 <CAS1>
A;Cross-references: UNIPARC:UPI00001737ED; EMBL:X57954; NID:g32150
A;Note: this allele is designated A*0204
A;Note: the sequence in GenBank entry HSHLAA020, release 106.0, (PID:g32151) differs bec
R;Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.; i

```


Nature 357, 326-329, 1992
A;Title: Unusual HLA-B alleles in two tribes of Brazilian Indians.
A;Reference number: 137120; MUID:92269955; PMID:1317015
A;Accession: S77965
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-365 <BBL>
A;Cross-references: UNIPARC:UPI0000124E24; EMBL:M84379; NID:g403143; PIDN:AAA59606.1; PI
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
R;Castano, A.R.; Lopez de Castro, J.A.
Immunogenetics 35, 344-346, 1992
A;Title: Structure of the HLA-A *0211 (A2.5) subtype: further evidence for selection-dri
A;Reference number: S23593; MUID:92218010; PMID:1559719
A;Accession: S23593
A;Molecule type: mRNA
A;Residues: 9-96; ID: 99-365 <CAS2>
A;Cross-references: UNIPARC:UPI000008AF57; EMBL:X60764; NID:g32156; PIDN:CAB56609.1; PID
A;Note: this allele is designated A*0211 (previously HLA-A2.5)
R;Orr, H.T.; Lopez de Castro, J.A.; Parham, P.; Ploegh, H.L.; Strominger, J.L.
Proc. Natl. Acad. Sci. U.S.A. 76, 4395-4399, 1979
A;Title: Comparison of amino acid sequences of two human histocompatibility antigens, HL
A;Reference number: A93834; MUID:80056745; PMID:92029
A;Accession: A93834
A;Molecule type: protein
A;Residues: 25-55, 'Z', 57-60, 'B', 64-66, 'Z', 68-74, 'X', 76-85, 'RXXX', 90-94, 'AH', 97, 'V'
A;Cross-references: UNIPARC:UPI00001737EE
A;Note: this sequence has been revised in reference A93919
R;Lopez de Castro, J.A.; Strominger, J.L.; Strong, D.M.; Orr, H.T.
Proc. Natl. Acad. Sci. U.S.A. 79, 3813-3817, 1982
A;Title: Structure of crossreactive human histocompatibility antigens HLA-A28 and HLA-A2
A;Reference number: A93919; MUID:82247941; PMID:6179086
A;Accession: A93919
A;Molecule type: protein
A;Residues: 25-85, 'RXXX', 90-94, 'AH', 97, 'V', 99-112, 'Z', 114-118, 'LZ', 121-125, 'X', 127-131, '
'232-265, 'E', 267-294 <LOP>
A;Cross-references: UNIPARC:UPI00001737EF
R;Silver, M.L.; Parker, K.C.; Wiley, D.C.
Nature 350, 619-622, 1991
A;Title: Reconstitution by MHC-restricted peptides of HLA-A2 heavy chain with beta-2-mic
A;Reference number: S14802; MUID:91204056; PMID:2017257
A;Accession: S14802
A;Molecule type: protein
A;Residues: 25-36 <SLI>
A;Cross-references: UNIPARC:UPI00001737FO
C;Genetics:
A;Gene: GDB:HLA-A
A;Cross-references: GDB:119310; OMIM:142800
A;Map position: 6p21.3-6p21.3
A;Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1; 365/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterodimer; transmembrane protein; transplanta
F;1-24/DNA: signal sequence #status predicted <SIG>
F;25-365/Product: MHC class I histocompatibility antigen HLA-A2 alpha chain #status expe
F;25-114/DNA: alpha-1 <EX1>
F;115-206/DNA: alpha-2 <EX2>
F;120-285/DNA: immunoglobulin homology <IMM>
F;307-331/DNA: transmembrane #status predicted <TM>
F;332-365/DNA: intracellular #status predicted <INT>
F;110/Binding site: carbohydrate (Aen) (covalent) #status experimental
F;125-188, 227-283/disulfide bonds: #status predicted

Query Match 44.9%; Score 44; DB 1; Length 365;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 6 IGSIRWFIRAFY 17
DB 127 VGSDFRFLRGYH 138

RESULT 7
138443

gene HLA-A-0203 protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: I38443
R;Holmes, N.; Ennis, P.; Wan, A.M.; Denney, D.W.; Parham, P.
J. Immunol. 139, 936-941, 1987
A;Title: Multiple genetic mechanisms have contributed to the generation of the HLA-A2/A28
A;Reference number: I38441; MUID:97252273; PMID:3496393
A;Accession: I38443
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-365 <RES>
A;Cross-references: UNIPARC:UPI000016A05E; EMBL:U03863; NID:g432438; PIDN:AAA03604.1; PI
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/DNA: immunoglobulin homology <IMM>

Query Match 44.9%; Score 44; DB 2; Length 365;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 6 IGSIRWFIRAFY 17
DB 127 VGSDFRFLRGYH 138

RESULT 8
161902
MHC class I histocompatibility antigen HLA-A alpha chain precursor - human (isolate A*021
C;Species: Homo sapiens (man)
A;Variety: isolate A*0212
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 23-Jul-1999
C;Accession: I61902
R;Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.; I
Nature 357, 326-329, 1992
A;Title: Unusual HLA-B alleles in two tribes of Brazilian Indians.
A;Reference number: I37120; MUID:92269955; PMID:1317015
A;Accession: I61902
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-365 <RES>
A;Cross-references: UNIPARC:UPI000016AD39; GB:M84378; NID:g187625; PIDN:AAA59604.1; PID:5
A;Experimental source: cell line KRC 033; isolate A*0212
C;Genetics:
A;Gene: GDB:HLA-A
A;Cross-references: GDB:119310; OMIM:142800
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: transmembrane protein
F;1-24/DNA: signal sequence #status predicted <SIG>
F;25-365/Product: MHC class I histocompatibility antigen HLA-A alpha chain #status predic
F;220-285/DNA: immunoglobulin homology <IMM>

Query Match 44.9%; Score 44; DB 2; Length 365;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 6 IGSIRWFIRAFY 17
DB 127 VGSDFRFLRGYH 138

RESULT 9
137542
MHC class I histocompatibility antigen HLA-A2 alpha chain (allele A*0216) precursor - hun
C;Species: Homo sapiens (man)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C;Accession: I37542; S49582
R;Barouch, D.; Krausa, P.; Bodmer, J.; Browning, M.J.; McMichael, A.J.
Immunogenetics 41, 388, 1995
A;Title: Identification of a novel HLA-A2 subtype, HLA-A*0216.
A;Reference number: I37542; MUID:95278976; PMID:7759139
A;Accession: I37542
A;Status: preliminary; translated from GB/EMBL/DBJ

```
A;Molecule type: mRNA
A;Residues: 1-365 <RES>
A;Cross-references: UNIPARC:UPI000016AA63; EMBL:Z46633; NID:g575248; PIDN:CAA86602.1; PID:
A;Note: submitted to the EMBL Data Library, November 1994
C;Genetics:
A;Gene: hla-A
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match      44.9%; Score 44; DB 2; Length 365;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      6 IGSIWRFIRAFY 17
      :||| |||:|:
Db      127 VGSDWRFRLRGYH 138

RESULT 10
I84448
MHC class I histocompatibility antigen HLA-A alpha chain precursor - human (isolate A*0211)
A;Species: Homo sapiens (man)
A;Variety: isolate A*0211
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999
C;Accession: I84448
R;Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.;
Nature 357, 326-329, 1992
A;Title: Unusual HLA-B alleles in two tribes of Brazilian Indians.
A;Reference number: I37120; MUID:92269955; PMID:1317015
A;Accession: I84448
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-365 <RES>
A;Cross-references: UNIPARC:UPI000016AD38; GB:M84377; NID:g187623; PIDN:AAA59603.1; PID:
A;Experimental source: cell line GRC 138; isolate A*0211
C;Genetics:
A;Gene: GDB:HLA-A
A;Cross-references: GDB:119310; OMIM:142800
A;Map position: gp21.3-gp21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-365/Product: MHC class I histocompatibility antigen HLA-A alpha chain #status predicted
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match      44.9%; Score 44; DB 2; Length 365;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      6 IGSIWRFIRAFY 17
      :||| |||:|:
Db      127 VGSDWRFRLRGYH 138

RESULT 11
I61857
MHC HLA-A2.4a chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I61857
R;Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
J. Immunol. 142, 3937-3950, 1989
A;Title: Diversity and diversification of HLA-A,B,C alleles.
A;Reference number: I36956; MUID:89235215; PMID:2715640
A;Accession: I61857
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-365 <RES>
A;Cross-references: UNIPARC:UPI000016AD48; GB:M24042; NID:g187777; PIDN:
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match      44.9%; Score 44; DB 2; Length 365;
```

```
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      6 IGSIWRFIRAFY 17
      :||| |||:|:
Db      127 VGSDWRFRLRGYH 138

RESULT 12
I38442
Gene HLA-A-0205 protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I38442
R;Holmes, N.; Ennis, P.; Wan, A.M.; Denney, D.W.; Parham, P.
J. Immunol. 139, 936-941, 1987
A;Title: Multiple genetic mechanisms have contributed to the generation of the HLA-A2/A28
A;Reference number: I38441; MUID:87252273; PMID:3496393
A;Accession: I38442
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-365 <RES>
A;Cross-references: UNIPROT:P01892; UNIPARC:UPI000016A06D; EMBL:U03862; NID:g432436; PIDN:
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match      44.9%; Score 44; DB 2; Length 365;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      6 IGSIWRFIRAFY 17
      :||| |||:|:
Db      127 VGSDWRFRLRGYH 138

RESULT 13
A34341
poly(3-hydroxybutyrate) synthase (EC 2.3.1.-) - Alcaligenes eutrophus
C;Species: Alcaligenes eutrophus
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C;Accession: A34341; A39190
R;Peoples, O.P.; Sinskey, A.J.
J. Biol. Chem. 264, 15298-15303, 1989
A;Title: Poly-beta-hydroxybutyrate (PHB) biosynthesis in Alcaligenes eutrophus H16. Ident
A;Reference number: A34341; MUID:89359357; PMID:2670936
A;Accession: A34341
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-589 <PEO>
A;Cross-references: UNIPROT:P23608; UNIPARC:UPI0000044953; GB:J05003; NID:g141958; PIDN:
A;Experimental source: strain H16
R;Schubert, P.; Krueger, N.; Steinbuechel, A.
J. Bacteriol. 173, 168-175, 1991
A;Title: Molecular analysis of the Alcaligenes eutrophus poly(3-hydroxybutyrate) biosynt
omoter.
A;Reference number: A39190; MUID:91100279; PMID:1987116
A;Accession: A39190
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-219 <SCH>
A;Cross-references: UNIPARC:UPI000016E162; GB:M64341; NID:g141964; PIDN:AAA21979.1; PID:
A;Note: the authors translated the codon TAC for residue 120 as Thr
C;Superfamily: poly(3-hydroxyalkanoic acid) synthase phbc
C;Keywords: acyltransferase

Query Match      44.9%; Score 44; DB 2; Length 589;
Best Local Similarity 47.6%; Pred. No. 34;
Matches 10; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

QY      3 RRFIGSIW-----RPIAFY 17
      ||| ||| ||| |||
Db      100 RRFAGDAWRTNLPYRFAAFY 120
```

RESULT 14

B81690
 Probable sodium-translocating NADH dehydrogenase (ubiquinone) (EC 1.6.5.-) nqrB chain TC
 C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C;Accession: B81690
 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, A.C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 A;Reference number: A81500; MUID:20150255; PMID:10684935
 A;Accession: B81690
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-503 <TET>
 A;Cross-references: UNIPROT:Q9PKB6; UNIPARC:UPI0000057982; GB:AE002323; GB:AE002160; NID
 A;Experimental source: strain Nigg (MoPn)
 C;Genetics:
 A;Gene: TC0550
 C;Keywords: oxidoreductase

Query Match 43.9%; Score 43; DB 2; Length 503;

Best Local Similarity 46.2%; Pred. No. 42;

Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 LRRFGSIWRFIR 14

Db 2 LKFPVDSLWKFGR 14

RESULT 15

T02263
 Cytochrome P450 DWARF3 - maize
 N;Contains: oxidoreductase (EC 1.-.-.-)
 C;Species: Zea mays (maize)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: T02263
 R;Winkler, R.G.; Helentjaris, T.
 Plant Cell 7, 1307-1317, 1995
 A;Title: The maize dwarf3 gene encodes a cytochrome P450-mediated early step in gibberellin biosynthesis
 A;Reference number: Z14648; MUID:96004534; PMID:7549486
 A;Accession: T02263
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-519 <WIN>
 A;Cross-references: UNIPROT:Q43246; UNIPARC:UPI0000126CF8; EMBL:U32579; NID:g987266; PID
 A;Experimental source: strain B73
 C;Genetics:
 A;Gene: dwarf3
 C;Function:
 A;Description: involved in an early step in gibberellin biosynthesis
 A;Pathway: gibberellin biosynthesis
 C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology
 C;Keywords: oxidoreductase
 F;325-488/Domain: cytochrome P450 homology <P45>

Query Match 43.9%; Score 43; DB 1; Length 519;

Best Local Similarity 54.5%; Pred. No. 43;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 IGSIWRFIRAF 16

Db 82 VGGMWAFLRAF 92

Search completed: May 19, 2006, 14:39:58

Job time : 15.2857 secs

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:13:32 ; Search time 115.429 seconds
(without alignments)
144.247 Million cell updates/sec

Title: US-10-712-447-116

Perfect score: 98

Sequence: 1 GLRRFGSIWRIFAFVG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	55.1	670	Q25271 LEPDE	Q25271 leptinotars
2	54	55.1	805	Q3APY5_CHLCH	Q3apy5 chlorobium
3	51	52.0	488	Q842W1_PEA	Q842w1 pisum sativ
4	50	51.0	735	Q3F7V7_RHILV	Q3f7v7 rhizobium 1
5	48	49.0	361	Q2NBS5_SODGL	Q2nbs5 sodalis glo
6	48	49.0	401	Q7NKW3_GLOVI	Q7nkw3 gloebacter
7	48	49.0	449	Q3PK79_PARDE	Q3pk79 paracoccus
8	48	49.0	579	1 XKR7_HUMAN	Q5gh72 homo sapien
9	48	49.0	579	1 XKR7_PANTR	Q491e1 pan troglod
10	48	49.0	580	1 XKR7_MOUSE	Q5gh64 mus musculu
11	48	49.0	580	1 XKR7_RAT	Q5gh56 rattus norv
12	48	49.0	597	2 Q5AUS5_EMENI	Q5aus5 aspergillus
13	48	49.0	627	2 P74489_SYNY3	P74489 synechocyst
14	48	49.0	805	2 Q44QD1_CHILLI	Q44qd1 chlorobium
15	48	49.0	815	2 Q43K01_9CHLB	Q43k01 chlorobium
16	47	48.0	219	2 Q6L1T5_PICTO	Q6l1t5 picrophilus
17	47	48.0	287	2 Q76442_CABEL	Q76442 caenorhabdi
18	47	48.0	407	2 Q39L57_BURS3	Q39l57 burkholderi
19	47	48.0	408	2 Q456F4_9BURK	Q456f4 burkholderi
20	47	48.0	408	2 Q4LK44_9BURK	Q4lk44 burkholderi
21	47	48.0	486	2 Q5U414_YENLA	Q5u414 xenopus lae
22	47	48.0	487	2 Q32N49_YENLA	Q32n49 xenopus lae
23	47	48.0	506	2 Q5VRM7_ORISA	Q5vrm7 oryza sativ
24	47	48.0	607	2 Q425W5_DESHA	Q425w5 desulfitoba
25	46	46.9	426	2 Q99A07_9VIRU	Q99a07 torque teno
26	46	46.9	578	1 XKR6_TETNG	Q491s8 tetraodon n
27	46	46.9	578	2 Q5GH49_FUGRU	Q5gh49 fugu rubrip
28	46	46.9	836	2 Q2Y8V4_NITMU	Q2y8v4 nitrosospir
29	45	45.9	278	2 Q7VW93_BORPE	Q7vw93 bordetella
30	45	45.9	278	2 Q7W7P3_BORPA	Q7w7p3 bordetella
31	45	45.9	278	2 Q7WL31_BORBR	Q7wl31 bordetella

32	45	45.9	376	2	Q8KBA7_CHLTE	Q8kba7 chlorobium
33	45	45.9	406	2	Q56YS1_ARATH	Q56ys1 arabidopsis
34	45	45.9	409	2	Q4BFM2_BURVI	Q4bfm2 burkholderi
35	45	45.9	435	2	Q2JIT0_9CVAN	Q2jit0 cyanobacter
36	45	45.9	458	2	Q3M6C5_ANAVT	Q3m6c5 anabaena va
37	45	45.9	458	2	Q8XG08_RALSO	Q8xg08 ralstonia s
38	45	45.9	489	1	KA02_ARATH	Q9c5y2 arabidopsis
39	45	45.9	490	2	Q842W0_PEA	Q842w0 pisum sativ
40	45	45.9	513	2	Q00857_FUSSP	Q00857 fusarium sp
41	45	45.9	519	2	Q9C1B7_FUSAR	Q9c1b7 fusarium sp
42	45	45.9	540	2	Q5GH65_MOUSE	Q5gh65 mus musculu
43	45	45.9	580	2	Q5GH40_BRARE	Q5gh40 brachydanio
44	45	45.9	638	1	XKR6_RAT	Q5gh57 rattus norv
45	45	45.9	641	1	XKR6_HUMAN	Q5gh73 homo sapien

ALIGNMENTS

RESULT 1
Q25271 LEPDE
ID Q25271 LEPDE PRELIMINARY; PRT; 670 AA.
AC Q25271; 1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Diapause protein 1 (Fragment).
GN Names: Dp19;
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pserygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Chrysomeloidea; Chrysomelidae; Chrysomelinae; Doryphorini;
OC Leptinotarsa.
OX NCBI_TaxID=7539;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA de Kort C.A.D., Koopmanschap A.B.;
RT "Nucleotide and deduced amino acid sequence of a cDNA clone encoding
RT diapause protein 1, an amylphorin-type storage hexamer of the Colorado
RT potato beetle.";
RL J. Insect Physiol. 40:527-535(1994).
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License

EMBL; X76080; CAA53691.1; -; mRNA.
HSP; P04253; ILLI.
GO; GO:0005344; F: oxygen transporter activity; IEA.
GO; GO:0006810; P: transport; IEA.
InterPro; IPR000896; Hemocyanin.
InterPro; IPR005203; hemocyanin C.
InterPro; IPR005204; hemocyanin N.
PANTHER; PTHR11511; Hemocyanin; 1.
Pfam; PF03723; Hemocyanin C; 1.
Pfam; PF00372; Hemocyanin M; 1.
Pfam; PF03722; Hemocyanin N; 1.
PRINTS; PR00187; HAEMOCYANIN.
PROSITE; PS00210; HEMOCYANIN_2; UNKNOWN_1.
NON_TER 1
SEQUENCE 670 AA; 79825 MW; 8A000BA15BEC8A6 CRC64;

Query Match 55.1%; Score 54; DB 2; Length 670;

Best Local Similarity 43.8%; Pred. No. 9.8;

Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 3 RRFSGSIWRIFAFVG 18

| | | | | | | | | | | | | | | | | |

Db 351 RKFYGALWSYLRHFFPG 366

RESULT 2

Q3APY5_CHLCH

ID Q3APY5_CHLCH PRELIMINARY; PRT; 805 AA.

AC Q3APV5;
 DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
 DT 22-NOV-2005, sequence version 1.
 DT 21-FEB-2006, entry version 5.
 DE Leucyl-tRNA synthetase class Ia (EC 6.1.1.4).
 GN OrderedLocusNames=Cag_1688;
 OS Chlorobium chlorochromatii (strain Cd3).
 OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
 OC Chlorobium/Pelodicyston group; Chlorobium.
 RN NCBI_TaxID=340177;
 RX [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RA US DOE Joint Genome Institute;
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
 RA Hammon N., Israni S., Pitluck S., Bryant D., Schmutz J., Larimer F.,
 RA Land M., Kyrpides N., Ivanova N., Richardson P.;
 RL "Complete sequence of Chlorobium chlorochromatii Cd3.";
 RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC EMBL: CP00108; AB28940.1; -; Genomic_DNA.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004823; F:leucine-tRNA ligase activity; IEA.
 DR GO: GO:0016874; F:ligase activity; IEA.
 DR GO: GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
 KW Aminoacyl-tRNA synthetase; Complete proteome; Ligase.
 SQ SEQUENCE 805 AA; 92007 MW; A0C78B83732AF54C CRC64;
 OS Chlorobium leguminosarum bv. viciae.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=387;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=305;
 RX MEDLINE=21360352; PubMed=11467725; DOI=10.1139/cjm-47-6-495;
 RA Venter A.P., Twelker S., Oresnik I.J., Hynes M.F.;
 RL "Analysis of the genetic region encoding a novel rhizobiotin from
 RT Rhizobium leguminosarum bv. viciae strain 305.";
 RL Can. J. Microbiol. 47:495-502(2001).
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC EMBL: AF273216; AAG25076.1; -; Genomic_DNA.
 DR HSPSP; P08716; IMT0.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0016887; F:ATPase activity; IEA.
 DR GO: GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO: GO:0000166; F:nucleotide binding; IEA.
 DR GO: GO:0008233; F:peptidase activity; IEA.
 DR GO: GO:0008565; F:protein transporter activity; IEA.
 DR GO: GO:0015031; P:protein transport; IEA.
 DR GO: GO:0006508; P:proteolysis; IEA.
 DR InterPro: IPR003593; AAA_Arpase.
 DR InterPro: IPR011527; ABC_TM_1.
 DR InterPro: IPR001140; ABC_TM_transp.
 DR InterPro: IPR003439; ABC_transp_like.
 DR InterPro: IPR005074; Peptidase_C39.
 DR InterPro: IPR010132; Type_I_sec_HlyB.
 DR PANTHER: PTHR1942:SF74; Type_I_sec_HlyB; 1.
 DR Pfam: PF00664; ABC_membrane; 1.
 DR Pfam: PF00005; ABC_tran; 1.
 DR Pfam: PF03412; Peptidase_C39; 1.
 DR ProDom: PD000006; ABC_transporter; 1.
 DR SMART: SM00382; AAA_1.
 DR TIGRFAMs: TIGR01846; Type_I_sec_HlyB; 1.
 DR PROSITE: PS0929; ABC_TM1F; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE: PS0893; ABC_TRANSPORTER_2; 1.

AC Q3APV5;
 DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
 DT 22-NOV-2005, sequence version 1.
 DT 21-FEB-2006, entry version 5.
 DE Leucyl-tRNA synthetase class Ia (EC 6.1.1.4).
 GN OrderedLocusNames=Cag_1688;
 OS Chlorobium chlorochromatii (strain Cd3).
 OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
 OC Chlorobium/Pelodicyston group; Chlorobium.
 RN NCBI_TaxID=340177;
 RX [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RA US DOE Joint Genome Institute;
 RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
 RA Hammon N., Israni S., Pitluck S., Bryant D., Schmutz J., Larimer F.,
 RA Land M., Kyrpides N., Ivanova N., Richardson P.;
 RL "Complete sequence of Chlorobium chlorochromatii Cd3.";
 RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC EMBL: CP00108; AB28940.1; -; Genomic_DNA.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004823; F:leucine-tRNA ligase activity; IEA.
 DR GO: GO:0016874; F:ligase activity; IEA.
 DR GO: GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
 KW Aminoacyl-tRNA synthetase; Complete proteome; Ligase.
 SQ SEQUENCE 805 AA; 92007 MW; A0C78B83732AF54C CRC64;
 OS Chlorobium leguminosarum bv. viciae.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=387;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=305;
 RX MEDLINE=21360352; PubMed=11467725; DOI=10.1139/cjm-47-6-495;
 RA Venter A.P., Twelker S., Oresnik I.J., Hynes M.F.;
 RL "Analysis of the genetic region encoding a novel rhizobiotin from
 RT Rhizobium leguminosarum bv. viciae strain 305.";
 RL Can. J. Microbiol. 47:495-502(2001).
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC EMBL: AF273216; AAG25076.1; -; Genomic_DNA.
 DR HSPSP; P08716; IMT0.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0016887; F:ATPase activity; IEA.
 DR GO: GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO: GO:0000166; F:nucleotide binding; IEA.
 DR GO: GO:0008233; F:peptidase activity; IEA.
 DR GO: GO:0008565; F:protein transporter activity; IEA.
 DR GO: GO:0015031; P:protein transport; IEA.
 DR GO: GO:0006508; P:proteolysis; IEA.
 DR InterPro: IPR003593; AAA_Arpase.
 DR InterPro: IPR011527; ABC_TM_1.
 DR InterPro: IPR001140; ABC_TM_transp.
 DR InterPro: IPR003439; ABC_transp_like.
 DR InterPro: IPR005074; Peptidase_C39.
 DR InterPro: IPR010132; Type_I_sec_HlyB.
 DR PANTHER: PTHR1942:SF74; Type_I_sec_HlyB; 1.
 DR Pfam: PF00664; ABC_membrane; 1.
 DR Pfam: PF00005; ABC_tran; 1.
 DR Pfam: PF03412; Peptidase_C39; 1.
 DR ProDom: PD000006; ABC_transporter; 1.
 DR SMART: SM00382; AAA_1.
 DR TIGRFAMs: TIGR01846; Type_I_sec_HlyB; 1.
 DR PROSITE: PS0929; ABC_TM1F; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE: PS0893; ABC_TRANSPORTER_2; 1.

DR GO: GO:0006118; P:electron transport; IEA.
 DR InterPro: IPR001128; Cytochrome_P450.
 DR InterPro: IPR002401; EP450I.
 DR PANTHER: PTHR19383; Cytochrome_P450; 1.
 DR Pfam: PF00067; P450; 2.
 DR PRINTS: PR00463; EP450I.
 DR PRINTS: PR00385; P450.
 DR PROSITE: PS00086; CYTOCHROME_P450; UNKNOWN_1.
 KW Endoplasmic reticulum; Heme; Iron; Membrane; Metal-binding;
 KW Monooxygenase; Oxidoreductase.
 SQ SEQUENCE 488 AA; 56478 MW; 503453CB6E43C830 CRC64;
 OS Rhizobium leguminosarum bv. viciae.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=387;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=305;
 RX MEDLINE=21360352; PubMed=11467725; DOI=10.1139/cjm-47-6-495;
 RA Venter A.P., Twelker S., Oresnik I.J., Hynes M.F.;
 RL "Analysis of the genetic region encoding a novel rhizobiotin from
 RT Rhizobium leguminosarum bv. viciae strain 305.";
 RL Can. J. Microbiol. 47:495-502(2001).
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC EMBL: AF273216; AAG25076.1; -; Genomic_DNA.
 DR HSPSP; P08716; IMT0.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0016887; F:ATPase activity; IEA.
 DR GO: GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO: GO:0000166; F:nucleotide binding; IEA.
 DR GO: GO:0008233; F:peptidase activity; IEA.
 DR GO: GO:0008565; F:protein transporter activity; IEA.
 DR GO: GO:0015031; P:protein transport; IEA.
 DR GO: GO:0006508; P:proteolysis; IEA.
 DR InterPro: IPR003593; AAA_Arpase.
 DR InterPro: IPR011527; ABC_TM_1.
 DR InterPro: IPR001140; ABC_TM_transp.
 DR InterPro: IPR003439; ABC_transp_like.
 DR InterPro: IPR005074; Peptidase_C39.
 DR InterPro: IPR010132; Type_I_sec_HlyB.
 DR PANTHER: PTHR1942:SF74; Type_I_sec_HlyB; 1.
 DR Pfam: PF00664; ABC_membrane; 1.
 DR Pfam: PF00005; ABC_tran; 1.
 DR Pfam: PF03412; Peptidase_C39; 1.
 DR ProDom: PD000006; ABC_transporter; 1.
 DR SMART: SM00382; AAA_1.
 DR TIGRFAMs: TIGR01846; Type_I_sec_HlyB; 1.
 DR PROSITE: PS0929; ABC_TM1F; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE: PS0893; ABC_TRANSPORTER_2; 1.

US DOE Joint Genome Institute;

```
DR PROSITE; PS50990; PEPTIDASE C39; 1.
SQ SEQUENCE 735 AA; 80717 MW; 0216259241F3630C CRC64;

Query Match 51.0%; Score 50; DB 2; Length 735;
Best Local Similarity 56.2%; Pred. No. 47;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 GLRRFIGSIWRFIRAF 16
   |||:||||:||||
Db 161 GFRWFLPAIWRYRAP 176

RESULT 5
ID Q2NUB5_SODGL PRELIMINARY; PRT; 361 AA.
AC Q2NUB5;
DT 07-FEB-2006, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DT 07-MAR-2006, entry version 2.
DE Putative glycosyltransferase.
GN ORFNames=SG0985;
OS Sodalitis glossinidius str. 'morsitans'.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Sodalitis.
OX NCBI_TaxID=343509;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Morsitans;
RA Toh H., Weiss B.L., Perkin S.A.H., Yamashita A., Oshima K.,
RA Hattori M., Aksoy S.;
RT "Massive genome erosion and functional adaptations provide insights
RT into the symbiotic lifestyle of Sodalitis glossinidius in the tsetse
RT host.";
RL Genome Res. 16:149-156 (2006).
CC
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AP008232; BAE74260.1; -; Genomic_DNA.
KW Transferase.
SQ SEQUENCE 361 AA; 40247 MW; 125770F3C3CA6EC CRC64;

Query Match 49.0%; Score 48; DB 2; Length 361;
Best Local Similarity 61.5%; Pred. No. 47;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 RFIGSIWRFIRAF 16
   |||:||||:|
Db 62 RDVGFWRFILSAF 74

RESULT 6
Q7NKW3_GLOVI
ID Q7NKW3_GLOVI PRELIMINARY; PRT; 401 AA.
AC Q7NKW3;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Gll1363 protein.
GN OrderedLocusNames=gll1363;
OS Gloeobacter violaceus.
OC Bacteria; Cyanobacteria; Gloeobacteria; Gloeobacteriales; Gloeobacter.
OX NCBI_TaxID=333072;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=PCC 7421;
RX MEDLINE=22977040; PubMed=14621292; DOI=10.1093/dnares/10.4.137;
RA Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,
RA Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimo S.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a
RT cyanobacterium that lacks thylakoids.";
```

```
RL DNA Res. 10:137-145 (2003).
CC
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; BA000045; BAC89304.1; -; Genomic_DNA.
DR BioCyc; GVIO251221:GLU1363-MONOMER; -.
DR GO; GO:0004040; F:amidase activity; IEA.
DR GO; GO:0008745; F:N-acetylglucosyl-L-alanine amidase activity; IEA.
DR GO; GO:0009253; P:peptidoglycan catabolism; IEA.
DR InterPro; IPR002508; Amidase_3_hydro.
DR InterPro; IPR002901; Amidase_4.
DR Pfam; PF01520; Amidase_3; 1.
DR Pfam; PF01832; Glucosaminidase; 1.
KW Complete proteome.
SQ SEQUENCE 401 AA; 44051 MW; 903814BB688C170B CRC64;

Query Match 49.0%; Score 48; DB 2; Length 401;
Best Local Similarity 69.2%; Pred. No. 52;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GLRRFIGSIWRFI 13
   |||:||||:|
Db 104 GLERFIRGYWRFI 116

RESULT 7
Q3PK79_PARDE
ID Q3PK79_PARDE PRELIMINARY; PRT; 449 AA.
AC Q3PK79;
DT 25-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Cytochrome P450.
GN ORFNames=PdenDRAFT_4722;
OS Paracoccus denitrificans PD1222.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Paracoccus.
OX NCBI_TaxID=318586;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PD1222;
RA US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Terani S., Pitluck S., Richardson P.;
RA "Sequencing of the draft genome and assembly of Paracoccus
RA denitrificans PD1222.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PD1222;
RA US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RA "Annotation of the draft genome assembly of Paracoccus denitrificans
RA PD1222.";
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -! SIMILARITY: Belongs to the cytochrome P450 family.
CC
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL; AA0701000001; EAN68115.1; -; Genomic_DNA.
DR GO; GO:0020037; F:heme binding; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002401; EP4501.
DR Pfam; PF00067; p450; 1.
```

```
DR PRINTS; PR00463; EP4501.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWNV.1.
KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase.
SQ SEQUENCE 449 AA; 50659 MW; 5F3BEC9E12AA3B35 CRC64;

Query Match 49.0%; Score 48; DB 2; Length 449;
Best Local Similarity 80.0%; Pred. No. 59;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 GSIWRFIRAF 16
Db 13 GSVWRIRDF 22

RESULT 8
XKR7 HUMAN
ID XKR7_HUMAN STANDARD; PRT; 579 AA.
AC Q5GH72; O9NUG5;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE XK-related protein 7.
DE Name=XKR7; Synonyms=C20orf159, XRG7;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Huang C.-H., Chen Y.;
RT "A superfamily of XK-related genes (XRG) widely expressed in
RT vertebrates and invertebrates.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/41485a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavridis G., Almeida J.P., Babbage A.K., Baggeley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark A., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Copley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhali P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leharasaiho M.H., Leverha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McKay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -1- SIMILARITY. Belongs to the XK family.
CC -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous
CC gene model prediction.
-----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
```

```
CC
DR EMBL; AY534245; AAT07094.1; -; mRNA.
DR EMBL; AL031658; CAB86102.1; ALT_SEQ; Genomic_DNA.
DR Ensembl; ENSG00000101321; Homo sapiens.
KW HGNC; HGNC:23062; XKR7.
KW Membrane; Transmembrane.
FT CHAIN 1 579
FT TRANSMEM 59 79
FT TRANSMEM 89 109
FT TRANSMEM 260 280
FT TRANSMEM 314 334
FT TRANSMEM 355 375
FT TRANSMEM 384 404
FT TRANSMEM 415 435
SQ SEQUENCE 579 AA; 63826 MW; D8D0FF64B9BDD53D CRC64;

Query Match 49.0%; Score 48; DB 1; Length 579;
Best Local Similarity 50.0%; Pred. No. 77;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSWRFIRAF 17
Db 190 LGQVWRYRLALY 201

RESULT 9
XKR7_PANTR
ID XKR7_PANTR STANDARD; PRT; 579 AA.
AC Q49LS1;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE XK-related protein 7.
DE Name=XKR7; Synonyms=XRG7;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pan.
OX NCBI_TaxID=9598;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Huang C.-H., Chen Y.;
RT "A superfamily of XK-related genes (XRG) widely expressed in
RT vertebrates and invertebrates.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -1- SIMILARITY. Belongs to the XK family.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
-----
CC
DR EMBL; AY702910; AAV83783.1; -; mRNA.
KW Membrane; Transmembrane.
FT CHAIN 1 579
FT TRANSMEM 59 79
FT TRANSMEM 89 109
FT TRANSMEM 260 280
FT TRANSMEM 314 334
FT TRANSMEM 355 375
FT TRANSMEM 384 404
FT TRANSMEM 415 435
SQ SEQUENCE 579 AA; 63593 MW; 6DFE1191093E85D4 CRC64;

Query Match 49.0%; Score 48; DB 1; Length 579;
Best Local Similarity 50.0%; Pred. No. 77;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSWRFIRAF 17
Db 190 LGQVWRYRLALY 201
```



```

RC STRAIN=DSM 245;
RG US DOE Joint Genome Institute (JGI-PGFI);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RT Hammon N., Istrani S., Pitluck S., Richardson P.;
RA "Sequencing of the draft genome and assembly of Chlorobium limicola
RT DSM 245.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 245;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Chlorobium limicola DSM
RL 245.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AAHQJ01000009; EAM43320.1; -; Genomic_DNA.
CC GO; GO:0005524; F:ATP binding; IEA.
CC GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
CC GO; GO:0006429; F:leucyl-tRNA aminoacylation; IEA.
CC InterPro; IPR002302; Leu_tRNAsyn_1a.
CC Pfam; PF00133; tRNA-synt_1; 1.
CC PRINTS; PR00985; TRNASYNTHLEU.
CC TIGRFAMs; TIGR00396; leuS_bact; 1.
CC Aminoacyl-tRNA synthetase.
CC SEQUENCE 805 AA; 91997 MW; D4F3FE28F9E92DF3 CRC64;
SQ
QY Query Match 49.0%; Score 48; DB 2; Length 805;
DB Best Local Similarity 46.2%; Pred.No. 1.1e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 GLRRFFIGSIWRFI 13
   |:|:|:|:|:
DB 622 GISRFLGKVRLV 634

RESULT 15
Q43K01_9CHLB Q43K01_9CHLB PRELIMINARY; PRT; 816 AA.
AC Q43K01_
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 21-FEB-2006, entry version 9.
DE Leucyl-tRNA synthetase bacterial/mitochondrial, class Ia.
DE ORFNames=Cpha266DRAFT_2546;
OS Chlorobium phaeobacteroides DSM 266.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium/Pelodictyon group; Chlorobium.
OX NCBI_TaxID=290317;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 266;
RG US DOE Joint Genome Institute (JGI-PGFI);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RT Hammon N., Istrani S., Pitluck S., Richardson P.;
RA "Sequencing of the draft genome and assembly of Chlorobium
RT phaeobacteroides DSM 266.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 266;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Chlorobium
RL phaeobacteroides DSM 266.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an

```

```
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AAIB01000002; EAM35935.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004823; F:leucine-tRNA ligase activity; IEA.
DR GO; GO:0006429; P:leucyl-tRNA aminoacylation; IEA.
DR InterPro; IPR002302; Leu_tRNAasn_la.
DR Pfam; PF00133; tRNA-synt_1; 1.
DR PRINTS; PRO0985; TRNASYNTHLEU.
DR TIGRFams; TIGR00396; leuS_bact; 1.
KW Aminoacyl-tRNA synthetase
SQ SEQUENCE 816 AA; 93335 MW; 6770B1DAC50560F1 CRC64;

Query Match 49.0%; Score 48; DB 2; Length 816;
Best Local Similarity 46.2%; Pred.No. 1.1e+02;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRPI 13
Db 622 GISRFLGKVRRLV 634
```

Search completed: May 19, 2006, 14:38:14
Job time : 116.429 secs

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:38:42 ; Search time 24.8571 Seconds
(without alignments)
63.384 Million cell updates/sec

Title: US-10-712-447-116

Perfect score: 98

Sequence: 1 GLRRFGSIWRIFAFVG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5 COMB.pep:*
 - 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.pep:*
 - 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.pep:*
 - 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB.pep:*
 - 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
 - 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE COMB.pep:*
 - 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	75.5	18	2	US-08-940-095-242
2	74	75.5	18	2	US-08-940-093-242
3	74	75.5	18	2	US-08-940-096-242
4	74	75.5	18	2	US-09-465-719-242
5	74	75.5	18	2	US-09-453-605-242
6	74	75.5	18	2	US-09-453-838-242
7	74	75.5	18	2	US-08-940-136-242
8	74	75.5	18	2	US-09-453-841-242
9	74	75.5	18	2	US-09-453-833-242
10	74	75.5	18	2	US-09-453-826-242
11	74	75.5	18	2	US-09-453-840-242
12	74	75.5	18	2	US-09-865-989-242
13	74	75.5	18	2	US-09-453-834-242
14	74	75.5	18	2	US-10-283-599-242
15	74	75.5	18	2	US-09-465-718-242
16	50	51.0	76	2	US-09-205-258-892
17	50	51.0	76	2	US-10-004-860-892
18	44	44.9	14	1	US-08-480-190-3
19	44	44.9	14	1	US-08-488-379-3
20	44	44.9	14	2	US-08-475-399A-3
21	44	44.9	14	2	US-08-077-255A-3
22	44	44.9	14	5	PCT-US93-07545-3
23	44	44.9	15	1	US-08-480-190-2
24	44	44.9	15	1	US-08-488-379-2
25	44	44.9	15	2	US-08-475-399A-2
26	44	44.9	15	2	US-08-077-255A-2

27	44	44.9	15	5	PCT-US93-07545-2	Sequence 2, Appli
28	44	44.9	18	1	US-08-480-190-1	Sequence 1, Appli
29	44	44.9	18	1	US-08-480-190-61	Sequence 61, Appli
30	44	44.9	18	1	US-08-488-379-1	Sequence 1, Appli
31	44	44.9	18	1	US-08-488-379-61	Sequence 61, Appli
32	44	44.9	18	2	US-08-475-399A-1	Sequence 1, Appli
33	44	44.9	18	2	US-08-475-399A-61	Sequence 61, Appli
34	44	44.9	18	2	US-08-077-255A-1	Sequence 1, Appli
35	44	44.9	18	2	US-08-077-255A-61	Sequence 61, Appli
36	44	44.9	18	5	PCT-US93-07545-1	Sequence 1, Appli
37	44	44.9	18	5	PCT-US93-07545-61	Sequence 61, Appli
38	44	44.9	156	2	US-09-513-999C-4289	Sequence 4289, Ap
39	44	44.9	182	1	US-08-127-954-137	Sequence 137, App
40	44	44.9	182	1	US-08-127-954-138	Sequence 138, App
41	44	44.9	182	1	US-08-127-954-139	Sequence 139, App
42	44	44.9	182	1	US-08-127-954-140	Sequence 140, App
43	44	44.9	182	1	US-08-127-954-141	Sequence 141, App
44	44	44.9	182	1	US-08-127-954-142	Sequence 142, App
45	44	44.9	182	1	US-08-127-954-144	Sequence 144, App

ALIGNMENTS

RESULT 1
US-08-940-095-242
; Sequence 242, Application US/08940095
; Patent No. 6004925
; GENERAL INFORMATION:
; APPLICANT: Daseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: ANOPIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DISLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,095
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6004925e
US-08-940-095-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11: Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRFIRAFYG 18
| : : | : | : | : | : | : |
Dd 1 GIKKELGSIWKFIKA FVG 18

RESULT 2
US-08-940-093-242
; Sequence 242, Application US/08940093
; Patent No. 6037323
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York

```
Query Match          75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11: Conservative 6; Mismatches 1; Indels 0; Gaps 0;
```

Qy 1 GLRRFIGSIWRFIRAFYG 18
|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFAVG 18

RESULT 3
US-08-940-096-242
; sequence 242, Application US/08940096
; Patent No. 6046166
; GENERAL INFORMATION:

```

/ APPLICANT: Dasseux, Jean-Louis
/
/ APPLICANT: Sekul, Renate
/
/ APPLICANT: Buttner, Klaus
/
/ APPLICANT: Cornut, Isabelle
/
/ APPLICANT: Metz, Gunther
/
/ TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
/
/ TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
/
/ NUMBER OF SEQUENCES: 258
/

```

Query Match	75.5%	Score 74;	DB 2;	Length 18;
Best Local Similarity	61.1%;	Pred. No. 3.9e-05;		
Marches 11: Conservative	6;	Mismatches 1;	Indels 0;	Gaps 0;

Qy 1 GLRRFIGSIWRFIRAFYG 18
| : : : | : : | : | : |
Dh 1 GIKKFI.GSIWKFIKAFVG 18

RESULT 4
US-09-465-719-242
; Sequence 242, Application US/09465719
; Patent No. 6265377
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
;

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/465,719
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,093
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6265377e
;
US-09-465-719-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRFIRAFVG 18
|:::|:::|:::|
Db 1 GIKKFLGSIWKFIRAFVG 18

RESULT 5
US-09-453-605-242
; Sequence 242, Application US/09453605
; Patent No. 6329341
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; Dufourcq, Jean
;
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,605
; FILING DATE: 26-NOV-1999
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
```

```
;
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6329341e
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:
;
US-09-453-605-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRFIRAFVG 18
|:::|:::|:::|
Db 1 GIKKFLGSIWKFIRAFVG 18

RESULT 6
US-09-453-838-242
; Sequence 242, Application US/09453838
; Patent No. 6376464
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
;
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,838
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6376464e
```

US-09-453-838-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLRRFTGSIWRFFIRAFVG 18
|:::|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 7

US-08-940-136-242

; Sequence 242, Application US/08940136
; Patent No. 6518412
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,136
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0007-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6518412e
; US-08-940-136-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLRRFTGSIWRFFIRAFVG 18
|:::|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 8

US-09-453-841-242

; Sequence 242, Application US/09453841

; Patent No. 6573239
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,841
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6573239e
; US-09-453-841-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLRRFTGSIWRFFIRAFVG 18
|:::|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 9

US-09-453-833-242

; Sequence 242, Application US/09453833
; Patent No. 6602854
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; US-09-453-833-242

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,833
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6602854e
US-09-453-833-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLRRFGSIWRFIRAFVG 18
|:::|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 10
US-09-453-826-242
Sequence 242, Application US/09453826
Patent No. 6630450
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,826
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6630450e
US-09-453-826-242
Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
QY 1 GLRRFGSIWRFIRAFVG 18
|:::|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18
RESULT 11
US-09-453-840-242
Sequence 242, Application US/09453840
Patent No. 6716816
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,840
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6716816e
US-09-453-840-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLRRFGSIWRFIRAFVG 18
|:::|:::|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 12

US-09-865-989-242
; Sequence 242, Application US/09865989
; Patent No. 6734169
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther

TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS

NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY

COUNTRY: USA
ZIP: 10036-2811

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/865,989
FILING DATE: 25-May-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/465,719
FILING DATE: 17-DEC-1999

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0006-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: No. 6734169e
SEQUENCE DESCRIPTION: SEQ ID NO: 242:
US-09-865-989-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLRRFGSIWRFIRAFVG 18
|:::|:::|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 13

US-09-453-834-242
; Sequence 242, Application US/09453834
; Patent No. 6753313
; GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean

TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY

COUNTRY: USA
ZIP: 10036-2811

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/453,834
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA: 08/940,095
APPLICATION NUMBER:
FILING DATE: 29-SEP-1997

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556

TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6753313e
US-09-453-834-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLRRFGSIWRFIRAFVG 18
|:::|:::|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 14

US-10-283-599-242
; Sequence 242, Application US/10283599
; Patent No. 6844327
; GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis
; Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean

TITLE OF INVENTION: GENE THERAPY APPROACHES TO
SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR

;; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
;; NUMBER OF SEQUENCES: 274
;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Pennie & Edmonds LLP
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: NY

;; COUNTRY: USA

;; ZIP: 10036-2811

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: DOS

;; SOFTWARE: FastSEQ Version 2.0

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/10/283,599

;; FILING DATE: 29-OCT-2002

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 08/940,136

;; FILING DATE: 29-SEP-1997

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Coruzzi, Laura A

;; REGISTRATION NUMBER: 30,742

;; REFERENCE/DOCKET NUMBER: 009196-0007-999

;; TELEPHONE: 650-493-4935

;; TELEFAX: 650-493-5556

;; TELEX: 66141 PENNIE

;; INFORMATION FOR SEQ ID NO: 242:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 18 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: No. 6844327e

;; US-10-283-599-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRPFIKAFVG 18

Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 15

US-09-465-718-242

;; Sequence 242, Application US/09465718

;; Patent No. 6900177

;; GENERAL INFORMATION:

;; APPLICANT: Dasseux, Jean-Louis

;; APPLICANT: Sekul, Renate

;; APPLICANT: Buttner, Klaus

;; APPLICANT: Cornut, Isabelle

;; APPLICANT: Metz, Gunther

;; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS

;; NUMBER OF SEQUENCES: 258

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Pennie & Edmonds LLP

;; STREET: 1155 Avenue of the Americas

;; CITY: New York

;; STATE: NY

;; COUNTRY: USA

;; ZIP: 10036-2811

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette

;; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: DOS

;; SOFTWARE: FastSEQ Version 2.0

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/465,718
;; FILING DATE: 17-Dec-1999

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US/08/940,096

;; FILING DATE: 29-SEP-1997

;; APPLICATION NUMBER:

;; FILING DATE:

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Coruzzi, Laura A

;; REGISTRATION NUMBER: 30,742

;; REFERENCE/DOCKET NUMBER: 009196-0005-999

;; TELEPHONE: 650-493-4935

;; TELEFAX: 650-493-5556

;; TELEX: 66141 PENNIE

;; INFORMATION FOR SEQ ID NO: 242:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 18 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: No. 6900177e

;; US-09-465-718-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 3.9e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRPFIKAFVG 18

Db 1 GIKKFLGSIWKFIKAFVG 18

Search completed: May 19, 2006, 14:42:55
Job time : 24.8571 secs

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 15:18:19 ; Search time 81.2857 seconds
(without alignments)
102.575 Million cell updates/sec

Title: US-10-712-447-116

Perfect score: 98
Sequence: 1 GLRRFIGSIWRFFRAFG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pgp.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pgp.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pgp.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_PUBCOMB.pgp.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pgp.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pgp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	18	4	US-10-712-447-115
2	98	100.0	18	4	US-10-712-447-116
3	94	95.9	18	4	US-10-712-447-2
4	94	95.9	18	4	US-10-712-447-5
5	94	95.9	18	4	US-10-712-447-8
6	94	95.9	18	4	US-10-712-447-10
7	94	95.9	18	4	US-10-712-447-13
8	94	95.9	18	4	US-10-712-447-117
9	94	95.9	18	4	US-10-712-447-127
10	94	95.9	18	4	US-10-712-447-131
11	91	92.9	18	4	US-10-712-447-91
12	90	91.8	18	4	US-10-712-447-129
13	88	89.8	18	4	US-10-712-447-21
14	88	89.8	18	4	US-10-712-447-53
15	88	89.8	18	4	US-10-712-447-74
16	86	87.8	18	4	US-10-712-447-4
17	86	87.8	18	4	US-10-712-447-112
18	86	87.7	18	4	US-10-712-447-99
19	84	85.7	18	4	US-10-712-447-18
20	84	85.7	18	4	US-10-712-447-113
21	84	85.7	18	4	US-10-712-447-114
22	83	84.7	18	4	US-10-712-447-17
23	83	84.7	18	4	US-10-712-447-121
24	82	83.7	18	4	US-10-712-447-61
25	82	83.7	18	4	US-10-712-447-82
26	81	82.7	18	4	US-10-712-447-16
27	81	82.7	18	4	US-10-712-447-96

28	80	81.6	18	4	US-10-712-447-22	Sequence 22, Appl
29	80	81.6	18	4	US-10-712-447-78	Sequence 78, Appl
30	80	81.6	18	4	US-10-712-447-95	Sequence 95, Appl
31	80	81.6	18	4	US-10-712-447-120	Sequence 120, Appl
32	78	79.6	18	4	US-10-712-447-19	Sequence 19, Appl
33	78	79.6	18	4	US-10-712-447-56	Sequence 56, Appl
34	78	79.6	18	4	US-10-712-447-58	Sequence 58, Appl
35	78	79.6	18	4	US-10-712-447-77	Sequence 77, Appl
36	78	79.6	18	4	US-10-712-447-79	Sequence 79, Appl
37	78	79.6	18	4	US-10-712-447-80	Sequence 80, Appl
38	78	79.6	18	4	US-10-712-447-94	Sequence 94, Appl
39	77	78.6	18	4	US-10-712-447-57	Sequence 57, Appl
40	77	78.6	18	4	US-10-712-447-100	Sequence 100, Appl
41	76	77.6	18	4	US-10-712-447-41	Sequence 41, Appl
42	76	77.6	18	4	US-10-712-447-119	Sequence 119, Appl
43	75	76.5	18	4	US-10-712-447-97	Sequence 97, Appl
44	74	75.5	18	3	US-09-865-989-242	Sequence 242, Appl
45	74	75.5	18	3	US-09-865-989-242	Sequence 242, Appl

ALIGNMENTS

RESULT 1
US-10-712-447-115
; Sequence 115, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 115
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; US-10-712-447-115

Query Match 100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRRFIGSIWRFFRAFG 18
| | | | | | | | | | | | | | | | | |
Db 1 GLRRFIGSIWRFFRAFG 18

RESULT 2
US-10-712-447-116
; Sequence 116, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13

```

RESULT 6
US-10-712-447-10
; Sequence 10, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETHA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712.447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 10
; LENGTH: 18

```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-10

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRFIRAFYG 18
   |:|:|:|:|:|:|:|:|:|
Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 7
US-10-712-447-13
; Sequence 13, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-13

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRFIRAFYG 18
   |:|:|:|:|:|:|:|:|:|
Db 1 GIRRFLGSIWRFIRAFYG 18

RESULT 8
US-10-712-447-117
; Sequence 117, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 117
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-117
```

```
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-117

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRFIRAFYG 18
   |:|:|:~:~:~:~:~:~:~:~:~
Db 1 GIRRFGSIWRFIRAFYG 18

RESULT 9
US-10-712-447-127
; Sequence 127, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 127
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-127

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLRRFGSIWRFIRAFYG 18
   |:|:~:~:~:~:~:~:~:~:~
Db 1 GLRRFGSIWRFIRAFYG 18

RESULT 10
US-10-712-447-131
; Sequence 131, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 131
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-131
```



```
; OTHER INFORMATION: (DiMe)Lys
US-10-712-447-53

Query Match      89.8%; Score 88; DB 4; Length 18;
Best Local Similarity 77.8%; Pred. No. 3.7e-06;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRRFIGSIWRIFAFYG 18
   |:|:|||||:||||
DB 1 GKRFGLGSIWRFKAFYG 18

RESULT 15
US-10-712-447-74
; Sequence 74, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHRAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123UUS
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 74
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-74

Query Match      89.8%; Score 88; DB 4; Length 18;
Best Local Similarity 77.8%; Pred. No. 3.7e-06;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLRRFIGSIWRIFAFYG 18
   |:|:|||||:||||
DB 1 GKRFGLGSIWRFKAFYG 18

Search completed: May 19, 2006, 15:27:57
Job time : 81.2857 secs
```

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 15:18:37 ; Search time 2.14286 Seconds
(without alignments)
17.943 Million cell updates/sec

Title: US-10-712-447-116

Perfect score: 98

Sequence: 1 GLRRFIGSIWRFIRAFVG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:

- 1: /EMC Celleria_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pbp.*
- 2: /EMC Celleria_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pbp.*
- 3: /EMC Celleria_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pbp.*
- 4: /EMC Celleria_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pbp.*
- 5: /EMC Celleria_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pbp.*
- 6: /EMC Celleria_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pbp.*
- 7: /EMC Celleria_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pbp.*
- 8: /EMC Celleria_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pbp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	38.8	74	1	US-09-949-925-111
2	37.5	38.3	441	6	US-10-511-937-2947
3	35	35.7	651	6	US-10-511-937-2401
4	34.5	35.2	60	1	US-09-949-925-142
5	34	34.7	522	6	US-10-505-928-543
6	34	34.7	599	7	US-11-302-678-5
7	33.5	34.2	244	7	US-11-169-140-109
8	33.5	34.2	503	7	US-11-024-544A-21
9	33.5	34.2	503	7	US-11-190-750-135
10	33.5	34.2	503	7	US-11-264-784-87
11	33	33.7	313	7	US-11-242-505A-48
12	33	33.7	342	7	US-11-204-427-7
13	33	33.7	393	7	US-11-304-129-40
14	33	33.7	403	7	US-11-304-129-48
15	33	33.7	403	7	US-11-242-505A-18
16	33	33.7	643	6	US-10-505-928-545
17	33	33.7	643	6	US-10-504-120-19
18	33	33.7	667	7	US-11-311-555-16
19	33	33.7	674	6	US-11-311-561-16
20	33	33.7	714	6	US-10-868-498-2
21	33	33.7	919	7	US-11-302-678-62
22	32	32.7	351	6	US-10-511-937-2540
23	32	32.7	364	7	US-11-113-081A-6
24	32	32.7	388	6	US-10-196-749-336
25	32	32.7	388	7	US-11-024-544A-169

26	32	32.7	388	7	US-11-190-750-137
27	32	32.7	388	7	US-11-204-427-1
28	32	32.7	423	7	US-11-312-958-12
29	32	32.7	464	6	US-10-488-015-17
30	32	32.7	544	6	US-10-505-928-859
31	32	32.7	627	7	US-11-249-111-88
32	32	32.7	747	7	US-11-261-384-2
33	32	32.7	764	7	US-11-223-738-6
34	31.5	32.1	4590	6	US-10-505-928-569
35	31	31.6	126	7	US-11-075-891-23
36	31	31.6	166	7	US-11-280-997-1
37	31	31.6	166	7	US-11-280-997-2
38	31	31.6	166	7	US-11-280-997-3
39	31	31.6	166	7	US-11-280-997-23
40	31	31.6	166	7	US-11-280-997-24
41	31	31.6	166	7	US-11-280-997-25
42	31	31.6	166	7	US-11-280-997-26
43	31	31.6	187	7	US-11-183-218-6
44	31	31.6	581	7	US-11-251-465-18
45	31	31.6	630	7	US-11-146-700-3

ALIGNMENTS

RESULT 1
US-09-949-925-111
Sequence 111, Application US/09949925
Publication No. US2006009575A9
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 67 Human secreted proteins
FILE REFERENCE: P2023P2
CURRENT APPLICATION NUMBER: US/09/949,925
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US 60/232,150
PRIOR FILING DATE: 2000-12-09
PRIOR APPLICATION NUMBER: PCT/US99/01621
PRIOR FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: US 60/073,160
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: US 60/073,159
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: US 60/073,165
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: US 60/073,164
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: US 60/073,167
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: US 60/073,162
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: US 60/073,161
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: US 60/073,170
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 298
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 111
LENGTH: 74
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (74)
OTHER INFORMATION: Xaa equals stop translation
US-09-949-925-111

Query Match 38.8%; Score 38; DB 1; Length 74;
Best Local Similarity 63.6%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 LRRFIGSIWRF 12

|||||

; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 543
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-543

Query Match 34.7%; Score 34; DB 6; Length 522;
Best Local Similarity 47.1%; Pred. No. 55;
Matches 8; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

Qy 3 RRPI-GSIWRFTRAFY 17
Db 473 RRFTQSGDLRHKHF 489
||| |::|||
||| |::|||

RESULT 6

US-11-302-678-5
; Sequence 5, Application US/11302678
; Publication No. US20060088881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46556, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: MPI02-012P1RNM OMNI
; CURRENT APPLICATION NUMBER: US/11/302,678
; CURRENT FILING DATE: 2005-12-14
; PRIOR APPLICATION NUMBER: US/10/345,680
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-302-678-5

Query Match 34.7%; Score 34; DB 7; Length 599;
Best Local Similarity 57.1%; Pred. No. 64;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 6 IGSIWRF 12
Db 64 LGNVWRF 70
:|::|||

RESULT 7

US-11-169-140-109

; Sequence 109, Application US/11169140
; Publication No. US20060099150A1
; GENERAL INFORMATION:
; APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
; APPLICANT: HOUSTON, Lou L.
; APPLICANT: SHERIDAN, Philip, J.
; APPLICANT: HAWLEY, Stephen
; APPLICANT: GLYNN, Jacqueline, M.
; APPLICANT: CHAPIN, Steven
; TITLE OF INVENTION: METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE AGENTS ACROSS CBI
; TITLE OF INVENTION: BARRIERS
; FILE REFERENCE: 11474-037-999
; CURRENT APPLICATION NUMBER: US/11/169,140
; CURRENT FILING DATE: 2005-06-27
; PRIOR APPLICATION NUMBER: US 60/267,601
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/248,819
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/248,478
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 60/237,929
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/949,039
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 09/969,748
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 109
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Simian
US-11-169-140-109

Query Match 34.2%; Score 33.5; DB 7; Length 244;
Best Local Similarity 42.1%; Pred. No. 27;
Matches 8; Conservative 3; Mismatches 3; Indels 5; Gaps 1;

Qy 1 GLRRFIGSIW----RFR 14
Db 158 GLVLALGAVNCVARFIR 176
||| |::|||

RESULT 8

US-11-024-544A-21
; Sequence 21, Application US/11024544A
; Publication No. US20060094086A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Yadav, Narendra
; APPLICANT: Xue, Zhixiong
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: DIACYLGLYCEROL ACYLTRANSFERASES FOR ALTERATION OF POLYUNSATURATED
; TITLE OF INVENTION: FATTY ACIDS AND OIL CONTENT IN OLEAGINOUS ORGANISMS
; FILE REFERENCE: CL2717
; CURRENT APPLICATION NUMBER: US/11/024,544A
; CURRENT FILING DATE: 2004-12-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 21
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Magnaporthe grisea 70-15
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank Accession No. EAA52634
; DATABASE ENTRY DATE: 2003-10-31
; RELEVANT RESIDUES: (1)..(503)
US-11-024-544A-21

Query Match 34.2%; Score 33.5; DB 7; Length 503;
Best Local Similarity 43.8%; Pred. No. 64;
Matches 7; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 3 RRFISWRFIRAFY 18
|||: ||: |
Db 156 RRFV-STWKLIALVHG 170

RESULT 9
US-11-190-750-135
; Sequence 135, Application US/11190750
; Publication No. US20060094089A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Yadav, Narendra
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: ACYTRANSFERRASE REGULATION TO INCREASE THE PERCENT OF
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN TOTAL LIPIDS AND OILS OF
; TITLE OF INVENTION: OLEAGINOUS ORGANISMS
; FILE REFERENCE: CL2718
; CURRENT APPLICATION NUMBER: US/11/190,750
; CURRENT FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 135
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Magnaporthe grisea 70-15 [GenBank Accession No. EAA52634]
US-11-190-750-135

Query Match 34.2%; Score 33.5; DB 7; Length 503;
Best Local Similarity 43.8%; Pred. No. 64;
Matches 7; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 3 RRFISWRFIRAFY 18
|||: ||: |
Db 156 RRFV-STWKLIALVHG 170

RESULT 10
US-11-264-784-87
; Sequence 87, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gallies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 87
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Magnaporthe grisea 70-15 [GenBank Accession No. EAA52634]
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: DGAT1
US-11-264-784-87

Query Match 34.2%; Score 33.5; DB 7; Length 503;
Best Local Similarity 43.8%; Pred. No. 64;
Matches 7; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 3 RRFISWRFIRAFY 18

Db 156 RRFV-STWKLIALVHG 170
|||: ||: |
|||: ||: |

RESULT 11
US-11-242-505A-48
; Sequence 48, Application US/11242505A
; Publication No. US20060099656A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310, 5
; FILE REFERENCE: MPI2001-288P1RCPIOMNIM
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-242-505A-48

Query Match 33.7%; Score 33; DB 7; Length 313;
Best Local Similarity 62.5%; Pred. No. 45;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 WRFIRAFY 17
|||: ||: |
Db 199 WSFLDAFY 206

RESULT 12
US-11-204-427-7
; Sequence 7, Application US/11204427
; Publication No. US20060100146A1
; GENERAL INFORMATION:
; APPLICANT: Sturley, Stephen L
; APPLICANT: Turkish, Aaron R
; APPLICANT: Billheimer, Jeffrey T
; APPLICANT: Cromley, Debra
; TITLE OF INVENTION: AWAT-RELATED METHODS AND ARTICLES
; FILE REFERENCE: 0575/72796/JPW/AJM/JCS
; CURRENT APPLICATION NUMBER: US/11/204,427
; CURRENT FILING DATE: 2005-08-15
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-204-427-7

Query Match 33.7%; Score 33; DB 7; Length 342;
Best Local Similarity 50.0%; Pred. No. 50;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 8 SWRFIRAFY 17
|||: ||: |
Db 84 AIWRLRDYI 93

RESULT 13

US-11-304-129-40
 ; Sequence 40, Application US/11304129
 ; Publication No. US20060088915A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OHTAKI, Tetsuya
 ; APPLICANT: MASUDA, Yasushi
 ; APPLICANT: TAKATSU, Yoshihiro
 ; APPLICANT: WATANABE, Takuya
 ; APPLICANT: TERAQ, Yasuko
 ; APPLICANT: SHINTANI, Yasushi
 ; APPLICANT: HINUMA, Syuji
 ; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
 ; FILE REFERENCE: 2762USOP
 ; CURRENT APPLICATION NUMBER: US/11/304,129
 ; CURRENT FILING DATE: 2005-12-15
 ; PRIOR APPLICATION NUMBER: US/10/333,192
 ; PRIOR FILING DATE: 2003-09-29
 ; PRIOR APPLICATION NUMBER: JP 2000-217442
 ; PRIOR FILING DATE: 2000-07-18
 ; PRIOR APPLICATION NUMBER: JP 2001-26779
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: PCT/JP01/06162
 ; PRIOR FILING DATE: 2001-07-17
 ; NUMBER OF SEQ ID NOS: 58
 ; SEQ ID NO 40
 ; LENGTH: 393
 ; TYPE: PRT
 ; ORGANISM: Rat
 ; US-11-304-129-40

Query Match 33.7%; Score 33; DB 7; Length 393;
 Best Local Similarity 46.2%; Pred. No. 58;
 Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 FIGSIWRFIRAFY 17
 | | | | : | |
 Db 216 FCGIWPVDQIFY 228

RESULT 14
 US-11-304-129-48
 ; Sequence 48, Application US/11304129
 ; Publication No. US20060088915A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OHTAKI, Tetsuya
 ; APPLICANT: MASUDA, Yasushi
 ; APPLICANT: TAKATSU, Yoshihiro
 ; APPLICANT: WATANABE, Takuya
 ; APPLICANT: TERAQ, Yasuko
 ; APPLICANT: SHINTANI, Yasushi
 ; APPLICANT: HINUMA, Syuji
 ; TITLE OF INVENTION: Novel Physiologically Active Peptide and Use Thereof
 ; FILE REFERENCE: 2762USOP
 ; CURRENT APPLICATION NUMBER: US/11/304,129
 ; CURRENT FILING DATE: 2005-12-15
 ; PRIOR APPLICATION NUMBER: US/10/333,192
 ; PRIOR FILING DATE: 2003-09-29
 ; PRIOR APPLICATION NUMBER: JP 2000-217442
 ; PRIOR FILING DATE: 2000-07-18
 ; PRIOR APPLICATION NUMBER: JP 2001-26779
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: PCT/JP01/06162
 ; PRIOR FILING DATE: 2001-07-17
 ; NUMBER OF SEQ ID NOS: 58
 ; SEQ ID NO 48
 ; LENGTH: 393
 ; TYPE: PRT
 ; ORGANISM: Mouse
 ; US-11-304-129-48

Query Match 33.7%; Score 33; DB 7; Length 393;
 Best Local Similarity 46.2%; Pred. No. 58;
 Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 5 FIGSIWRFIRAFY 17
 | | | | : | |
 Db 216 FCGIWPVDQIFY 228

RESULT 15
 US-11-242-505A-18
 ; Sequence 18, Application US/11242505A
 ; Publication No. US20060099656A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Carroll, Joseph M.
 ; APPLICANT: Healy, Aileen
 ; TITLE OF INVENTION: Methods and Compositions for Treating
 ; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
 ; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1380, 14717, 9941, 19310,
 ; FILE REFERENCE: MPI2001-288P1RCP10NMIM
 ; CURRENT APPLICATION NUMBER: US/11/242,505A
 ; CURRENT FILING DATE: 2005-10-03
 ; PRIOR APPLICATION NUMBER: US 10/290,078
 ; PRIOR FILING DATE: 2002-11-07
 ; PRIOR APPLICATION NUMBER: US 60/347,949
 ; PRIOR FILING DATE: 2001-11-07
 ; PRIOR APPLICATION NUMBER: US 10/320,351
 ; PRIOR FILING DATE: 2002-12-16
 ; PRIOR APPLICATION NUMBER: 60/341,606
 ; PRIOR FILING DATE: 2001-12-17
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 18
 ; LENGTH: 403
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; US-11-242-505A-18

Query Match 33.7%; Score 33; DB 7; Length 403;
 Best Local Similarity 44.4%; Pred. No. 60;
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LRRFIGSIW 10
 : | | : | : | |
 Db 155 VRRVLGAVW 163

Search completed: May 19, 2006, 15:28:18
 Job time : 3.14286 secs

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:13:22 ; Search time 94.2857 seconds
(without alignments)
87.287 Million cell updates/sec

Title: US-10-712-447-117

Perfect score: 98

Sequence: 1 GIRFIGSIWFLRAFGY 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq 8:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004as:*

9: Geneseqp2005as:*

10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	18	ADO34340	Synthetic
2	94	95.9	18	ADO34231	Synthetic
3	94	95.9	18	ADO34354	Synthetic
4	94	95.9	18	ADO34225	Synthetic
5	94	95.9	18	ADO34338	Synthetic
6	94	95.9	18	ADO34352	Synthetic
7	94	95.9	18	ADO34228	Synthetic
8	94	95.9	18	ADO34236	Synthetic
9	94	95.9	18	ADO34339	Synthetic
10	94	95.9	18	ADO34233	Synthetic
11	94	95.9	18	ADO34350	Synthetic
12	91	92.9	18	ADO34314	Synthetic
13	88	89.8	18	ADO34297	Synthetic
14	88	89.8	18	ADO34244	Synthetic
15	88	89.8	18	ADO34276	Synthetic
16	86	87.8	18	ADO34336	Synthetic
17	86	87.8	18	ADO34327	Synthetic
18	85	86.7	18	ADO34322	Synthetic
19	84	85.7	18	ADO34335	Synthetic
20	84	85.7	18	ADO34337	Synthetic
21	84	85.7	18	ADO34241	Synthetic
22	83	84.7	18	ADO34240	Synthetic
23	83	84.7	18	ADO34344	Synthetic

24	82	83.7	18	8	ADO34284	Ado34284 Synthetic
25	82	83.7	18	8	ADO34305	Ado34305 Synthetic
26	81	82.7	18	8	ADO34239	Ado34239 Synthetic
27	81	82.7	18	8	ADO34319	Ado34319 Synthetic
28	80	81.6	18	8	ADO34245	Ado34245 Synthetic
29	80	81.6	18	8	ADO34301	Ado34301 Synthetic
30	80	81.6	18	8	ADO34343	Ado34343 Synthetic
31	80	81.6	18	8	ADO34318	Ado34318 Synthetic
32	78	79.6	18	8	ADO34302	Ado34302 Synthetic
33	78	79.6	18	8	ADO34279	Ado34279 Synthetic
34	78	79.6	18	8	ADO34303	Ado34303 Synthetic
35	78	79.6	18	8	ADO34242	Ado34242 Synthetic
36	78	79.6	18	8	ADO34300	Ado34300 Synthetic
37	78	79.6	18	8	ADO34281	Ado34281 Synthetic
38	78	79.6	18	8	ADO34317	Ado34317 Synthetic
39	77	78.6	18	8	ADO34323	Ado34323 Synthetic
40	77	78.6	18	8	ADO34280	Ado34280 Synthetic
41	76	77.6	18	8	ADO34341	Ado34341 Synthetic
42	76	77.6	18	8	ADO34333	Ado34333 Synthetic
43	76	77.6	18	8	ADO34264	Ado34264 Synthetic
44	75	76.5	18	8	ADO34320	Ado34320 Synthetic
45	74	75.5	18	2	AAV18917	AAV18917 Lecithin:

ALIGNMENTS

RESULT 1

ADO34340
ID ADO34340 standard; peptide; 18 AA.

XX
AC ADO34340;

XX
DT 12-AUG-2004 (first entry)

XX
DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 117.

XX
KW apolipoprotein-E mimicking polypeptide; antilipemic; cardiactant;
KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX
OS Synthetic.

XX
PN WO2004043403-A2.

XX
PD 27-MAY-2004.

XX
PF 13-NOV-2003; 2003WO-US036268.

XX
PR 13-NOV-2002; 2002US-0425821P.

XX
PA (UABR-) UAB RES FOUND.

XX
PI Anantharamiah GM, Garber DW, Datta G;

XX
XX WPI; 2004-411629/38.

XX
DR Synthetic apolipoprotein-E mimicking polypeptide useful for treating
coronary artery disease, dysbetalipoproteinemia or atherosclerosis
comprises an amino acid sequence.

XX
PS Claim 4; SEQ ID NO 117; 79pp; English.

XX
CC The invention relates to a novel synthetic apolipoprotein-E mimicking
polypeptide. The invention further comprises an isolated nucleic acid
encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
a host cell, a recombinant cell or a transgenic, non-human subject
(including animal or plant) comprising the synthetic apolipoprotein-E
mimicking polypeptide encoding polynucleotide; a composition comprising
the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC angiainal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 SQ Sequence 18 AA;

Query Match 100.0%; Score 98; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.9e-08; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFIGSIWRFRAFYG 18
 |||||:|||||:|||||
 Db 1 GRRFIGSIWRFRAFYG 18

RESULT 2

ADO34231
 ID ADO34231 standard; peptide; 18 AA.

AC ADO34231;
 XX

DT 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 8.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; angiainal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 8; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC angiainal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFIGSIWRFRAFYG 18
 |||||:|||||:|||||
 Db 1 GRRFIGSIWRFRAFYG 18

RESULT 3

ADO34354
 ID ADO34354 standard; peptide; 18 AA.

XX ADO34354;
 XX

DT 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 131.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; angiainal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 131; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,

CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFIGSIWRFLRAFYG 18
 | : | | | : | | | | | | | | | | | | | |
 Db 1 GLRRFLGSIWRFLRAFYG 18

RESULT 4
 ADO34225
 ID ADO34225 standard; peptide; 18 AA.

AC ADO34225;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking polypeptide related R18L peptide.

KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 18 /note= "C-terminal amide"

FT WO2004043403-A2.

PN 27-MAY-2004.

PP 13-NOV-2003; 2003WO-US036268.

PR 13-NOV-2002; 2002US-0425821P.

PA (UABR-) UAB RES FOUND.

PI Anantharamiah GM, Garber DW, Datta G;

DR WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

PS Claim 4; SEQ ID NO 2; 79pp; English.

CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E

CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFIGSIWRFLRAFYG 18
 | : | | | : | | | | | | | | | | | | | |
 Db 1 GIRRFLGSIWRFLRAFYG 18

RESULT 5
 ADO34338
 ID ADO34338 standard; peptide; 18 AA.

XX ADO34338;

XX 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 115.

KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

PS Claim 4; SEQ ID NO 115; 79pp; English.

CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising

CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFIGSIWRFLRAFYG 18
 |.:|||||||.:|||
 Db 1 GLRRFIGSIWRFLRAFYG 18

RESULT 6
 ADO34352
 ID ADO34352 standard; peptide; 18 AA.

AC ADO34352;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 129.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 129; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFIGSIWRFLRAFYG 18
 |.:|||||||.:|||
 Db 1 GLRRFIGSIWRFLRAFYG 18

RESULT 7
 ADO34228
 ID ADO34228 standard; peptide; 18 AA.

AC ADO34228;

DT 12-AUG-2004 (first entry)

DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 5.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

OS Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 5; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX
 SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFIGSIWRFLRAFYG 18
 |||||:|||||:|||||
 Db 1 GIRRFLGSIWRFLRAFYG 18

RESULT 8
 ADO34236
 ID ADO34236 standard; peptide; 18 AA.

XX
 AC ADO34236;
 XX
 DT 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 13.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 13; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFIGSIWRFLRAFYG 18
 |||||:|||||:|||||
 Db 1 GIRRFLGSIWRFLRAFYG 18

RESULT 9
 ADO34339
 ID ADO34339 standard; peptide; 18 AA.

XX ADO34339;

XX 12-AUG-2004 (first entry)

XX Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 116.

XX apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX Synthetic.

XX WO2004043403-A2.

XX 27-MAY-2004.

XX 13-NOV-2003; 2003WO-US036268.

XX 13-NOV-2002; 2002US-0425821P.

XX (UABR-) UAB RES FOUND.

XX Anantharamiah GM, Garber DW, Datta G;

XX WPI; 2004-411629/38.

XX Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX Claim 4; SEQ ID NO 116; 79pp; English.

XX The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,

CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFTGSIWRFLRAFYG 18
 |:|||||:|||||
 Db 1 GLRRFTGSIWRFLRAFYG 18

RESULT 10

ADO34233
 ID ADO34233 standard; peptide; 18 AA.

XX AC ADO34233;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 10.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GW, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 10; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFTGSIWRFLRAFYG 18
 |:|||||:|||||
 Db 1 GLRRFTGSIWRFLRAFYG 18

RESULT 11

ADO34350
 ID ADO34350 standard; peptide; 18 AA.

XX AC ADO34350;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 127.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GW, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 127; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 95.9%; Score 94; DB 8; Length 18;
 Best Local Similarity 88.9%; Pred. No. 1.6e-07;
 Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFIGSLWRFLRAFYG 18
 |:|||||:|||||
 Db 1 GLRRFIGSLWRFLRAFYG 18

RESULT 12

ADO34314
 ID ADO34314 standard; peptide; 18 AA.

XX AC ADO34314;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 91.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 91; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal

CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
 CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX SQ Sequence 18 AA;

Query Match 92.9%; Score 91; DB 8; Length 18;
 Best Local Similarity 83.3%; Pred. No. 4.8e-07;
 Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFIGSLWRFLRAFYG 18
 |:|||||:|||||
 Db 1 GRRKFLGSLWRFLRAFYG 18

RESULT 13

ADO34297

ID ADO34297 standard; peptide; 18 AA.

XX AC ADO34297;

XX DT 12-AUG-2004 (first entry)

XX DE Synthetic apolipoprotein-E mimicking peptide, SEQ ID NO 74.

XX KW apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;
 KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;
 KW serum cholesterol; coronary artery disease; dysbetalipoproteinemia;
 KW atherosclerosis; myocardial infarction; stroke; embolus; angina;
 KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX OS Synthetic.

XX PN WO2004043403-A2.

XX PD 27-MAY-2004.

XX PF 13-NOV-2003; 2003WO-US036268.

XX PR 13-NOV-2002; 2002US-0425821P.

XX PA (UABR-) UAB RES FOUND.

XX PI Anantharamiah GM, Garber DW, Datta G;

XX DR WPI; 2004-411629/38.

XX PT Synthetic apolipoprotein-E mimicking polypeptide useful for treating
 PT coronary artery disease, dysbetalipoproteinemia or atherosclerosis
 PT comprises an amino acid sequence.

XX PS Claim 4; SEQ ID NO 74; 79pp; English.

XX CC The invention relates to a novel synthetic apolipoprotein-E mimicking
 CC polypeptide. The invention further comprises an isolated nucleic acid
 CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,
 CC a host cell, a recombinant cell or a transgenic, non-human subject
 CC (including animal or plant) comprising the synthetic apolipoprotein-E
 CC mimicking polypeptide encoding polynucleotide; a composition comprising
 CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and
 CC an monoclonal antibody that specifically binds to the synthetic
 CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E
 CC mimicking polypeptide has the following activities: antilipaeamic,
 CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and
 CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is
 CC useful for reducing serum cholesterol in a subject (including a mammal
 CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,

CC chimpanzee or orangutan); for treating coronary artery disease,
 CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 89.8%; Score 88; DB 8; Length 18;
 Best Local Similarity 77.8%; Pred. No. 1.4e-06;
 Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFSGIWRFLRAFYG 18
 ||||:|||||:||||
 Db 1 GIRKFLGSIWRFIKAFYG 18

RESULT 14
 ADO34244
 ID ADO34244 standard; peptide; 18 AA.

XX

AC ADO34244;

XX

12-AUG-2004 (first entry)

XX

Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 21.

XX

apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;

KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;

KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;

KW atherosclerosis; myocardial infarction; stroke; embolus; angina;

KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX

Synthetic.

XX

WO2004043403-A2.

XX

27-MAY-2004.

XX

13-NOV-2003; 2003WO-US036268.

XX

13-NOV-2002; 2002US-0425821P.

XX

(UABR-) UAB RES FOUND.

XX

Anantharamiah GM, Garber DW, Datta G;

XX

WPI; 2004-411629/38.

XX

Synthetic apolipoprotein-E mimicking polypeptide useful for treating

PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis

PT comprises an amino acid sequence.

XX

Claim 4; SEQ ID NO 21; 79pp; English.

XX

The invention relates to a novel synthetic apolipoprotein-E mimicking

CC polypeptide. The invention further comprises an isolated nucleic acid

CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,

CC a host cell, a recombinant cell or a transgenic, non-human subject

CC (including animal or plant) comprising the synthetic apolipoprotein-E

CC mimicking polypeptide encoding polynucleotide; a composition comprising

CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

CC an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipaeamic,

CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

CC useful for reducing serum cholesterol in a subject (including a mammal

CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,

CC chimpanzee or orangutan); for treating coronary artery disease,

CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
 CC myocardial infarction or stroke; for breaking an embolus in the subject;
 CC and also for treating angina. The synthetic apolipoprotein-E mimicking
 CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
 CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
 CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
 CC mimicking polypeptide of the invention.

XX Sequence 18 AA;

Query Match 89.8%; Score 88; DB 8; Length 18;
 Best Local Similarity 77.8%; Pred. No. 1.4e-06;
 Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIRRFSGIWRFLRAFYG 18
 ||||:|||||:||||
 Db 1 GIRKFLGAIWRFIRSFYG 18

RESULT 15
 ADO34276

ID ADO34276 standard; peptide; 18 AA.

XX

ADO34276;

XX

12-AUG-2004 (first entry)

XX

Synthetic apolipoprotein-E mimicking peptide, SEQ ID No 53.

XX

apolipoprotein-E mimicking polypeptide; antilipaeamic; cardiant;

KW vasotropic; antiarteriosclerotic; cerebroprotective; antianginal;

KW serum cholesterol; coronary artery disease; dysbetalipoproteinaemia;

KW atherosclerosis; myocardial infarction; stroke; embolus; angina;

KW low-density lipoprotein; LDL; very low density lipoprotein; VLDL.

XX

Synthetic.

XX

Key Location/Qualifiers

PH Modified-site 1..18

FT /note= "All Lys residues are DiMethyl-Lysine"

XX

WO2004043403-A2.

XX

27-MAY-2004.

XX

13-NOV-2003; 2003WO-US036268.

XX

13-NOV-2002; 2002US-0425821P.

XX

(UABR-) UAB RES FOUND.

XX

Anantharamiah GM, Garber DW, Datta G;

XX

WPI; 2004-411629/38.

XX

Synthetic apolipoprotein-E mimicking polypeptide useful for treating

PT coronary artery disease, dysbetalipoproteinaemia or atherosclerosis

PT comprises an amino acid sequence.

XX

Claim 4; SEQ ID NO 53; 79pp; English.

XX

The invention relates to a novel synthetic apolipoprotein-E mimicking

CC polypeptide. The invention further comprises an isolated nucleic acid

CC encoding the synthetic apolipoprotein-E mimicking polypeptide; a vector,

CC a host cell, a recombinant cell or a transgenic, non-human subject

CC (including animal or plant) comprising the synthetic apolipoprotein-E

CC mimicking polypeptide encoding polynucleotide; a composition comprising

CC the synthetic apolipoprotein-E mimicking polypeptide and a carrier; and

CC an monoclonal antibody that specifically binds to the synthetic

CC apolipoprotein-E mimicking polypeptide. The synthetic apolipoprotein-E

CC mimicking polypeptide has the following activities: antilipaeamic,

CC cardiant, vasotropic, antiarteriosclerotic, cerebroprotective, and

CC antianginal. The synthetic apolipoprotein-E mimicking polypeptide is

CC useful for reducing serum cholesterol in a subject (including a mammal

CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,

CC chimpanzee or orangutan); for treating coronary artery disease,

CC useful for reducing serum cholesterol in a subject (including a mammal
CC such as a mouse, rat, rabbit, cow, sheep, pig, human, monkey, ape,
CC chimpanzee or orangutan); for treating coronary artery disease,
CC dysbetalipoproteinaemia or atherosclerosis; and for reducing the risk of
CC myocardial infarction or stroke; for breaking an embolus in the subject;
CC and also for treating angina. The synthetic apolipoprotein-E mimicking
CC polypeptide enhances binding of low-density lipoprotein (LDL) or very low
CC density lipoprotein (VLDL) to a cell and enhances degradation of LDL or
CC VLDL by a cell. This sequence represents a synthetic apolipoprotein-E
CC mimicking polypeptide of the invention.

XX
SQ Sequence 18 AA;
Query Match 89.8%; Score 88; DB 8; Length 18;
Best Local Similarity 77.8%; Pred. No. 1.4e-06;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFIGSIWFLRAFYG 18
|||:|||||:|||||
Db 1 GIKRFLGSIWFLRAFYG 18

Search completed: May 19, 2006, 14:24:30
Job time : 94.2857 secs

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocollaboration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:24:57 ; Search time 14.2857 Seconds
(without alignments)
121.233 Million cell updates/sec

Title: US-10-712-447-117

Perfect score: 98

Sequence: 1 GIRRFIGSIWRFLEAFYFG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80:*

1: Pirl1.*

2: Pirl2.*

3: Pirl3.*

4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	48	49.0	627	2	S76462	hypothetical prote
2	47	48.0	489	2	B84733	probable cytochrom
3	46	46.9	246	2	I54412	MHC HLA-A cell sur
4	46	46.9	273	1	HLHU69	MHC class I histoc
5	46	46.9	365	1	HLHU2	MHC class I histoc
6	46	46.9	365	2	I38443	Gene HLA-A-0203 pr
7	46	46.9	365	2	I61902	MHC class I histoc
8	46	46.9	365	2	I37542	MHC class I histoc
9	46	46.9	365	2	I84448	MHC class I histoc
10	46	46.9	365	2	I61857	MHC HLA-A2.4a chai
11	46	46.9	365	2	I38442	gene HLA-A-0205 pr
12	46	46.9	516	2	T33269	hypothetical prote
13	45	45.9	519	1	T02263	cytochrome P450 DW
14	45	45.9	719	2	AG3325	DNA ligase (NAD) (
15	44.5	45.4	760	2	E84953	penicillin-binding
16	44	44.9	589	2	A34341	poly(3-hydroxybuty
17	44	44.9	806	2	A84060	leucyl-tRNA synthet
18	44	44.9	1112	2	T42383	probable calcium-a
19	43.5	44.4	790	2	T50337	homolog to drosoph
20	43	43.9	178	2	A75578	transcription regu
21	42.5	43.4	1025	2	AH3568	acriflavin resista
22	42	42.9	265	2	C42595	rfaP protein - Esc
23	42	42.9	426	2	B90410	hypothetical prote
24	42	42.9	803	2	A01282	leucyl-tRNA synthet
25	42	42.9	803	2	AH1653	leucyl-tRNA synthet
26	41.5	42.3	178	2	T19064	hypothetical prote
27	41	41.8	131	2	AG2115	hypothetical prote
28	41	41.8	207	2	D84114	galactosyltransfer
29	41	41.8	275	2	S21348	probable pol polyp

30 41 41.8 297 2 E97350
31 41 41.8 384 2 T08940
32 41 41.8 406 2 F96571
33 41 41.8 503 2 B81690
34 41 41.8 537 2 T04745
35 41 41.8 804 2 B89961
36 41 41.8 1003 2 S09145
37 40 40.8 107 2 T52113
38 40 40.8 127 2 B84023
39 40 40.8 139 2 G64032
40 40 40.8 228 2 T15530
41 40 40.8 231 2 F64842
42 40 40.8 237 2 B72892
43 40 40.8 374 2 F82993
44 40 40.8 411 2 AF2320
45 40 40.8 418 2 AD3417

ABC-type sugar tra
hypothetical prote
hypothetical prote
probable sodium-tr
hypothetical prote
leucyl-tRNA synthet
ND5 intron 4 prote
probable transcrip
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
probable permease
hypothetical prote
transporter, mfs s

ALIGNMENTS

RESULT 1

S76462

hypothetical protein - Synchocystis sp. (strain PCC 6803)

C:Species: Synchocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: S76462

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis

S.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S76462

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-627 <KAN>

A:Cross-references: UNIPROT:P74489; UNIPARC:UPI000000C103F; EMBL:D90915; GB:AB001339; NID:

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 49.0%; Score 48; DB 2; Length 627;

Best Local Similarity 38.9%; Pred. No. 8;

Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GIRRFIGSIWRFLEAFYFG 18

Db 597 GLEQLLGKIQWLNQKFG 614

RESULT 2

B84733

probable cytochrome P450 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: B84733

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.S.

guss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: B84733

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-489 <STO>

A:Cross-references: UNIPROT:Q9ZV72; UNIPARC:UPI0000009DBED; GB:AE002093; NID:g3831452; PII

C:Genetics:

A:Gene: At2g32440

A:Map position: 2

C:Superfamily: Synchocystis cytochrome P450 sl-0574; cytochrome P450 homology

Query Match 48.0%; Score 47; DB 2; Length 489;

```

Best Local Similarity 72.7%; Pred. No. 9;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 IGSIRFLRAP 16
   ||::|||
Db 54 IGNWSFLRAP 64

RESULT 3
I54412
MHC HLA-A cell surface antigen - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C:Accession: I54412
R:Arnot, D.; Lillie, J.W.; Auffray, C.; Kappes, D.; Strominger, J.L.
Immunogenetics 20, 237-252, 1984
A>Title: Inter-locus and intra-allelic polymorphisms of HLA class I antigen gene mRNA.
A:Reference number: I54412; MUID:84287690; PMID:6332068
A:Accession: I54412
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-246 <RES>
A:Cross-references: UNIPROT:Q29945; UNIPARC:UPI000008A27D; GB:M27537; NID:g187727; PIDN:
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: surface antigen
F:101-166/Domain: immunoglobulin homology <IMM>

Query Match 46.9%; Score 46; DB 2; Length 246;
Best Local Similarity 58.3%; Pred. No. 6.7;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSIRFLRAPY 17
   |||||::
Db 8 VGSDFRLRGYH 19

RESULT 4
HLH069
MHC class I histocompatibility antigen HLA-Aw69 alpha chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: B24671
R:Holmes, N.; Parham, P.
EMBO J. 4, 2849-2854, 1985
A>Title: Exon shuffling in vivo can generate novel HLA class I molecules.
A:Reference number: A91021; MUID:86055720; PMID:3877632
A:Accession: B24671
A:Molecule type: DNA
A:Residues: 1-273 <HOL>
A:Cross-references: UNIPROT:P10316; UNIPARC:UPI0000124E4B
C:Genetics:
A:Gene: GDB:HLA-A
A:Cross-references: GDB:119310; OMIM:142800
A:Map position: 6p21.3-6p21.3
A:Introns: 89/3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen
F:195-260/Domain: immunoglobulin homology <IMM>
F:85/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 46.9%; Score 46; DB 1; Length 273;
Best Local Similarity 59.3%; Pred. No. 7.4;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSIRFLRAPY 17
   |||||::
Db 102 VGSDFRLRGYH 113

RESULT 5
HLH0A2
MHC class I histocompatibility antigen HLA-A2 alpha chain precursor [validated] - human
C:Species: Homo sapiens (man)

```

```

C>Date: 28-Feb-1980 #sequence_revision 22-Apr-1995 #text_change 08-Dec-2000
C:Accession: I55948; E35997; A02191; S19020; S77965; S23593; A93834; A93919; S14802; A021
R:Koller, B.H.; Orr, H.T.
J. Immunol. 134, 2727-2733, 1985
A>Title: Cloning and complete sequence of an HLA-A2 gene: Analysis of two HLA-A alleles
A:Reference number: I55948; MUID:85132727; PMID:2982951
A:Accession: I55948
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-365 <KOL>
A:Cross-references: UNIPARC:UPI0000124E24; GB:K02883; NID:g187605; PIDN:AAA98727.1; PID:
R:Ennis, P.D.; Zemmour, J.; Salter, R.D.; Parham, P.
Proc. Natl. Acad. Sci. U.S.A. 87, 2833-2837, 1990
A>Title: Rapid cloning of HLA-A,B cDNA by using the polymerase chain reaction: frequency
A:Reference number: A35997; MUID:90207291; PMID:2320591
A:Accession: E35997
A:Molecule type: mRNA
A:Residues: 1-365 <ENN>
A:Cross-references: UNIPARC:UPI0000124E24; GB:M84379; GB:M32322; NID:g403143; PIDN:AAA59
A>Note: this allele is designated A*0201 (previously HLA-A2.1)
R:Kragel, M.S.
EMBO J. 4, 1205-1210, 1985
A>Title: Unusual RNA splicing generates a secreted form of HLA-A2 in a mutagenized B lymph
A:Reference number: A02191; MUID:85230571; PMID:3874058
A:Accession: A02191
A:Molecule type: mRNA
A:Residues: 39-365 <KRA>
A:Cross-references: UNIPARC:UPI000016AA56; GB:X02457; NID:g32153; PIDN:CAA26297.1; PID:
A>Note: the author translated the codon CAG for residue 96 as His, ACU for residue 97 as
s Thr, and ACU for residue 323 as Ser
R:Castano, A.R.; Lopez de Castro, J.A.
Immunogenetics 34, 281-285, 1991
A>Title: Structure of the HLA-A*0204 antigen, found in South American Indians. Spatial cl
A:Reference number: S19020; MUID:92039809; PMID:1937577
A:Accession: S19020
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 9-120, 'M', 122-365 <CAS1>
A:Cross-references: UNIPARC:UPI00001737ED; EMBL:X57954; NID:g32150
A>Note: this allele is designated A*0204
A>Note: the sequence in GenBank entry HSHLAA020, release 106.0, (PID:g32151) differs beca
R:Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.;
Nature 357, 326-329, 1992
A>Title: Unusual HLA-B alleles in two tribes of Brazilian Indians.
A:Reference number: I37120; MUID:92289555; PMID:1317015
A:Accession: S77965
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-365 <BEL>
A:Cross-references: UNIPARC:UPI0000124E24; EMBL:M84379; NID:g403143; PIDN:AAA59606.1; PI
A:Experimental source: cell line GRC 138; isolate A*0201
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
R:Castano, A.R.; Lopez de Castro, J.A.
Immunogenetics 35, 344-346, 1992
A>Title: Structure of the HLA-A*0211 (A2.5) subtype: further evidence for selection-driv
A:Reference number: S23593; MUID:92218010; PMID:1559719
A:Accession: S23593
A:Molecule type: mRNA
A:Residues: 9-96, 'ID', 99-365 <CAS2>
A:Cross-references: UNIPARC:UPI000008AF57; EMBL:X60764; NID:g32156; PIDN:CAB56609.1; PID:
A>Note: this allele is designated A*0211 (previously HLA-A2.5)
R:Orr, H.T.; Lopez de Castro, J.A.; Parham, P.; Ploegh, H.L.; Strominger, J.L.
Proc. Natl. Acad. Sci. U.S.A. 76, 4395-4399, 1979
A>Title: Comparison of amino acid sequences of two human histocompatibility antigens, HL
A:Reference number: A93834; MUID:80056745; PMID:92029
A:Accession: A93834
A:Molecule type: protein
A:Residues: 25-55, 'Z', 57-60, 'B', 62, 'B', 64-66, 'Z', 68-74, 'X', 76-85, 'RXXX', 90-94, 'AH', 97, 'V'
A:Cross-references: UNIPARC:UPI00001737EE
A>Note: this sequence has been revised in reference A93919
R:Lopez de Castro, J.A.; Strominger, J.L.; Strong, D.M.; Orr, H.T.
Proc. Natl. Acad. Sci. U.S.A. 79, 3813-3817, 1982

```

A;Title: Structure of crossreactive human histocompatibility antigens HLA-A28 and HLA-A2
A;Reference number: A93919; MUID:82247941; PMID:6179086
A;Accession: A93919
A;Molecule type: protein
A;Residues: 25-85; 'RXX', 90-94, 'AH', 97, 'V', 99-112, 'Z', 114-119, 'LZ', 121-125, 'X', 127-131, '232-265', 'B', 267-294 <LOP>
A;Cross-references: UNIPARC:UPI00001737EF
R;Silver, M.L.; Parker, K.C.; Wiley, D.C.
Nature 350, 619-622, 1991
A;Title: Reconstitution by MHC-restricted peptides of HLA-A2 heavy chain with beta-2-microglobulin
A;Reference number: S14802; MUID:91204056; PMID:2017257
A;Accession: S14802
A;Molecule type: protein
A;Residues: 25-36 <SIL>
A;Cross-references: UNIPARC:UPI00001737F0
C;Genetics:
A;Gene: GDB:HLA-A
A;Cross-references: GDB:119310; OMIM:142800
A;Map position: 6p21.3-6p21.3
A;Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1; 365/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterodimer; transmembrane protein; transplanted
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-365/Product: MHC class I histocompatibility antigen HLA-A2 alpha chain #status expected
F;25-114/Domain: alpha-1 <EX1>
F;115-206/Domain: alpha-2 <EX2>
F;220-285/Domain: immunoglobulin homology <IMM>
F;307-331/Domain: transmembrane #status predicted <TM>
F;332-365/Domain: intracellular #status predicted <INT>
F;110/Binding site: carbohydrate (asn) (covalent) #status experimental
F;125-188,227-283/Disulfide bonds: #status predicted

Query Match 46.9%; Score 46; DB 1; Length 365;
Best Local Similarity 58.3%; Pred. No. 9.8;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSWRFRLAFY 17
: || || || || :
DB 127 VGSDWRFRLRGYH 138

RESULT 6
I38443
gene HLA-A-0203 protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: I38443
R;Holmes, N.; Ennis, P.; Wan, A.M.; Denney, D.W.; Parham, P.
J. Immunol. 139, 936-941, 1987
A;Title: Multiple genetic mechanisms have contributed to the generation of the HLA-A2/A23
A;Reference number: I38441; MUID:87252273; PMID:3496393
A;Accession: I38443
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-365 <RES>
A;Cross-references: UNIPARC:UPI000016A06E; EMBL:U03863; NID:9432438; PIDN:AAA03604.1; PID:161902
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 46.9%; Score 46; DB 2; Length 365;
Best Local Similarity 58.3%; Pred. No. 9.8;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSWRFRLAFY 17
: || || || || :
DB 127 VGSDWRFRLRGYH 138

RESULT 7
161902
MHC class I histocompatibility antigen HLA-A alpha chain precursor - human (isolate A*0211)
C;Species: Homo sapiens (man)
A;Variety: isolate A*0211

C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 23-Jul-1999
C;Accession: I61902
R;Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.; I Nature 357, 326-329, 1992
A;Title: Unusual HLA-B alleles in two tribes of Brazilian Indians.
A;Reference number: I37120; MUID:92269955; PMID:1317015
A;Accession: I61902
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-365 <RES>
A;Cross-references: UNIPARC:UPI000016AD39; GB:M84378; NID:9187625; PIDN:AAA59604.1; PID:161902
A;Experimental source: cell line KRC 033; isolate A*0212
C;Genetics:
A;Gene: GDB:HLA-A
A;Cross-references: GDB:119310; OMIM:142800
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-365/Product: MHC class I histocompatibility antigen HLA-A alpha chain #status predicted
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 46.9%; Score 46; DB 2; Length 365;
Best Local Similarity 58.3%; Pred. No. 9.8;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSWRFRLAFY 17
: || || || || :
DB 127 VGSDWRFRLRGYH 138

RESULT 8
I37542
MHC class I histocompatibility antigen HLA-A2 alpha chain (allele A*0216) precursor - human
C;Species: Homo sapiens (man)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C;Accession: I37542; S49582
R;Barouch, D.; Krausa, P.; Bodmer, J.; Browning, M.J.; McMichael, A.J.
Immunogenetics 41, 388, 1995
A;Title: Identification of a novel HLA-A2 subtype, HLA-A*0216.
A;Reference number: I37542; MUID:95278976; PMID:7759139
A;Accession: I37542
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-365 <RES>
A;Cross-references: UNIPARC:UPI000016AA63; EMBL:Z46633; NID:9575248; PIDN:CAA86602.1; PID:161902
A;Note: submitted to the EMBL Data Library, November 1994
C;Genetics:
A;Gene: hla-A
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>

Query Match 46.9%; Score 46; DB 2; Length 365;
Best Local Similarity 58.3%; Pred. No. 9.8;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSWRFRLAFY 17
: || || || || :
DB 127 VGSDWRFRLRGYH 138

RESULT 9
I84448
MHC class I histocompatibility antigen HLA-A alpha chain precursor - human (isolate A*0211)
C;Species: Homo sapiens (man)
A;Variety: isolate A*0211
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999
C;Accession: I84448
R;Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz, R.; I Nature 357, 326-329, 1992
A;Title: Unusual HLA-B alleles in two tribes of Brazilian Indians.
A;Reference number: I37120; MUID:92269955; PMID:1317015
A;Accession: I84448

A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-365 <RES>
A;Cross-references: UNIPARC:UPI000016AD38; GB:M84377; NID:g187623; PIDN:AAAS9603.1; PID:
A;Experimental source: cell line GRC 138; isolate A*0211
C;Genetics:
A;Gene: GDB:HLA-A
A;Cross-references: GDB:119310; OMIM:142800
A;Map position: gp21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-365/Product: MHC class I histocompatibility antigen HLA-A alpha chain #status predicted
F;220-285/Domain: immunoglobulin homology <IMM>
Query Match 46.9%; Score 46; DB 2; Length 365;
Best Local Similarity 58.3%; Pred. No. 9.8;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 6 IGSIRWFLRAFY 17
Db 127 VGSDFRFLRGYH 138
::: ||||| :::
RESULT 10
I61857
MHC HLA-A2.4a chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I61857
R;Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
J. Immunol. 142, 3937-3950, 1989
A;Title: Diversity and diversification of HLA-A,B,C alleles.
A;Reference number: I36956; MUID:89235215; PMID:2715640
A;Accession: I61857
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-365 <RES>
A;Cross-references: UNIPROT:P01892; UNIPARC:UPI000016AD48; GB:M24042; NID:g187777; PIDN:
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>
Query Match 46.9%; Score 46; DB 2; Length 365;
Best Local Similarity 58.3%; Pred. No. 9.8;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 6 IGSIRWFLRAFY 17
Db 127 VGSDFRFLRGYH 138
::: ||||| :::
RESULT 11
I38442
gene HLA-A-0205 protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I38442
R;Holmes, N.; Ennis, P.; Wan, A.M.; Denney, D.W.; Parham, P.
J. Immunol. 139, 936-941, 1987
A;Title: Multiple genetic mechanisms have contributed to the generation of the HLA-A2/A2
A;Reference number: I38441; MUID:87252273; PMID:3496393
A;Accession: I38442
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-365 <RES>
A;Cross-references: UNIPROT:P01892; UNIPARC:UPI000016A06D; EMBL:U03862; NID:g432436; PID
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>
Query Match 46.9%; Score 46; DB 2; Length 365;
Best Local Similarity 58.3%; Pred. No. 9.8;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 IGSIRWFLRAFY 17
Db 127 VGSDFRFLRGYH 138
::: ||||| :::
RESULT 12
T33269
hypothetical protein C24B9.13 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33269
R;Murray, J.; Wohldmann, P.; Langston, Y.; O'Neal, D.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid C24B9.
A;Reference number: Z21310
A;Accession: T33269
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-516 <MUR>
A;Cross-references: UNIPROT:O76442; UNIPARC:UPI000007D477; EMBL:AF068709; PIDN:AAC19257.1
A;Experimental source: strain Bristol N2; clone C24B9
C;Genetics:
A;Gene: CESP:C24B9.13
A;Map position: 5
A;Introns: 13/3; 67/2; 116/2; 268/2; 315/2; 364/2
Query Match 46.9%; Score 46; DB 2; Length 516;
Best Local Similarity 47.1%; Pred. No. 14;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
Qy 2 IREFIGSIRWFLRAFYG 18
Db 252 LKFFITSLWMFMHAFDG 268
::: ||||| :::
RESULT 13
T02263
cytochrome P450 DWARF3 - maize
N;Contains: oxidoreductase (EC 1.-.-.-)
C;Species: Zea mays (maize)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: T02263
R;Winkler, R.G.; Helentjaris, T.
Plant Cell 7, 1307-1317, 1995
A;Title: The maize dwarf3 gene encodes a cytochrome P450-mediated early step in gibberellin
A;Reference number: Z14648; MUID:96004534; PMID:7549486
A;Accession: T02263
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-519 <WIN>
A;Cross-references: UNIPROT:Q43246; UNIPARC:UPI0000126CF8; EMBL:U32579; NID:g987266; PIDN:
A;Experimental source: strain B73
C;Genetics:
A;Gene: dwarf3
C;Function:
A;Description: involved in an early step in gibberellin biosynthesis
A;Pathway: gibberellin biosynthesis
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology
C;Keywords: oxidoreductase
F;325-488/Domain: cytochrome P450 homology <P45>
Query Match 45.9%; Score 45; DB 1; Length 519;
Best Local Similarity 63.6%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 6 IGSIRWFLRAF 16
Db 82 VGGWAFRAF 92
::: ||||| :::
RESULT 14
AG3325
DNA ligase (NAD) (EC 6.5.1.2) [imported] - Brucella melitensis (strain 16M)

C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 31-Dec-2004
C:Accession: AG3325
R:DeVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, E.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesha
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AG3325
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-719 <KUR>
A:Cross-references: UNIPROT:Q8YI56; UNIPARC:UPI0000057D37; GB:AE008917; PIDN:AAL51770.1;
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI0589
A:Map position: I
C:Superfamily: DNA ligase (NAD), Liga type
C:Keywords: ligase

Query Match 45.9%; Score 45; DB 2; Length 719;
Best Local Similarity 58.3%; Pred. No. 27;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IRRFIGSIWREL 13
Db 102 VRDFVGSVYREL 113
:|:|:|:|:|

RESULT 15
E84953
penicillin-binding protein 1b [imported] - Buchnera sp. (strain APS)
C:Species: Buchnera sp.
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C:Accession: E84953
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
A:Reference number: AB4930; MUID:20445173; PMID:10993077
A:Accession: E84953
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-760 <STO>
A:Cross-references: UNIPARC:UPI000005B4C8; GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
A:Gene: mrcB; BU200
C:Superfamily: penicillin-binding protein 1B

Query Match 45.4%; Score 44.5; DB 2; Length 760;
Best Local Similarity 50.0%; Pred. No. 35;
Matches 9; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Qy 2 IRRFI-GSIWRFLAFYG 18
Db 32 INRFNGKVNFPPTSIYG 49
| | | | | : | | | | |

Search completed: May 19, 2006, 14:39:57
Job time : 15.2857 secs

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 14:13:32 ; Search time 115.429 seconds
(without alignments)
144.247 Million cell updates/sec

Title: US-10-712-447-117
Perfect score: 98
Sequence: 1 GIRFFIGSIWFLRAFG 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	57.1	670	2	Q25271 LEPDE
2	54	55.1	805	2	Q3APY5 CHLCH
3	53	54.1	488	2	Q84ZW1 PEA
4	51	52.0	735	2	Q9F7V7 RHILV
5	50	51.0	361	2	Q2N8B5 SODGL
6	50	51.0	579	1	KKR7 HUMAN
7	50	51.0	579	1	KKR7 PANTR
8	50	51.0	580	1	KKR7 MOUSE
9	50	51.0	580	1	KKR7 RAT
10	49	50.0	278	2	Q7VV93 BORPE
11	49	50.0	278	2	Q7W7P3 BORPA
12	49	50.0	278	2	Q7WL31 BORBR
13	49	50.0	407	2	Q39L57 BURS3
14	49	50.0	408	2	Q456F4 9BURK
15	49	50.0	408	2	Q4LK44 9BURK
16	49	50.0	506	2	Q5VRM7 ORISA
17	48	49.0	188	2	Q2ILN7 9DELT
18	48	49.0	298	2	Q8R587 MOUSE
19	48	49.0	607	2	Q425W5 DESHA
20	48	49.0	627	2	P74489 SYNY3
21	48	49.0	805	2	Q44QD1 CHLLI
22	48	49.0	816	2	Q43K01 CHLORBI
23	47.5	48.5	577	2	Q36XB4 RHOPA
24	47.5	48.5	577	2	Q37C12 RHOPA
25	47	48.0	376	2	Q8KBA7 CHLTH
26	47	48.0	406	2	Q56YS1 ARATH
27	47	48.0	409	2	Q4BFM2 BURVI
28	47	48.0	486	2	Q5U4I4 XENLA
29	47	48.0	487	2	Q32N49 XENLA
30	47	48.0	489	1	KAO2 ARATH
31	47	48.0	490	2	Q84ZW0 PEA

32	47	48.0	597	2	Q5AUS5 EMENI
33	47	48.0	739	2	Q5NPG9 ZYMONA
34	46	46.9	18	2	Q9TNQ7 HUMAN
35	46	46.9	91	2	Q7YNX8 HUMAN
36	46	46.9	91	2	Q7YNY1 HUMAN
37	46	46.9	91	2	Q86IA8 HUMAN
38	46	46.9	91	2	Q8SNB2 HUMAN
39	46	46.9	162	2	Q4QYZ9 HUMAN
40	46	46.9	166	2	P79495 HUMAN
41	46	46.9	169	2	P78376 HUMAN
42	46	46.9	177	2	Q70PC8 HUMAN
43	46	46.9	180	2	Q5DSC6 HUMAN
44	46	46.9	181	2	O19520 HUMAN
45	46	46.9	181	2	O19671 HUMAN

ALIGNMENTS

RESULT 1
Q25271 LEPDE
ID Q25271_LEPDE PRELIMINARY; PRT; 670 AA.
AC Q25271, 1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE Diapause protein 1 (Fragment).
GN Name=Dp19;
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pserygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Chrysomeloidea; Chrysomelidae; Chrysomelinae; Doryphorini;
OC Leptinotarsa.
OX NCBI_TaxID=7539;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA de Kort C.A.B., Koopmanschap A.B.;
RT "Nucleotide and deduced amino acid sequence of a cDNA clone encoding diapause protein 1, an amylin-type storage hexamer of the Colorado potato beetle."
RL J. Insect Physiol. 40:527-535(1994).

CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
EMBL; X76080; CAA53691.1; -; mRNA.
DR HSSP; P04253; 1LL1.
DR GO; GO:0005344; F: oxygen transporter activity; IEA.
DR GO; GO:0006810; P: transport; IEA.
DR InterPro; IPR000896; Hemocyanin.
DR InterPro; IPR005203; hemocyanin C.
DR InterPro; IPR005204; hemocyanin N.
DR PANTHER; PTHR11511; Hemocyanin; 1.
DR Pfam; PF03723; Hemocyanin_C; 1.
DR Pfam; PF00372; Hemocyanin_M; 1.
DR Pfam; PF03722; Hemocyanin_N; 1.
DR PRINTS; PR00187; HAEMOCYANIN.
DR PROSITE; PS00210; HAEMOCYANIN_2; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 670 AA; 79825 MW; 8A000BA15B5C8A6 CRC64;

Query Match 57.1%; Score 56; DB 2; Length 670;

Best Local Similarity 50.0%; Pred. No. 4.3;

Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 3 RRFIGSIWFLRAFG 18

| : | : | : | : | : |

Db 351 RKFYGALMSYLRHFFG 366

RESULT 2

Q3APY5 CHLCH

ID Q3APY5_CHLCH PRELIMINARY; PRT; 805 AA.

```
AC Q3APV5;
DR 22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 22-NOV-2005, sequence version 1.
DT 21-FEB-2006, entry version 5.
DE Leucyl-tRNA synthetase class Ia (EC 6.1.1.4).
GN OrderedLocusNames=Cag.1688;
OS Chlorobium chlorochromatii (strain CaD3).
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium/Pelodictyon group; Chlorobium.
ON NCBI_TaxID=340177;
RX [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG US DOE Joint Genome Institute.
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C., Glavina T.,
RA Hammon N., Israni S., Picluk S., Bryant P., Schmutz J., Larimer F.,
RA Land M., Kyripides N., Ivanova N., Richardson P.,
RT "Complete sequence of Chlorobium chlorochromatii CaD3.";
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: CP000108; AB28940.1; -; Genomic_DNA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004823; F:leucine-tRNA ligase activity; IEA.
DR GO: GO:0016874; F:ligase activity; IEA.
DR GO: GO:0006429; F:leucyl-tRNA aminocyclization; IEA.
KW Aminoacyl-tRNA synthetase; Complete proteome; Ligase.
SQ SEQUENCE 805 AA; 92007 MW; A0C78B83732AF54C CRC64;

Query Match 55.1%; Score 54; DB 2; Length 805;
Best Local Similarity 61.5%; Pred. No. 11;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GIRRFIGSIWRFL 13
DB 622 GISRFLGKVRV 634

RESULT 3
Q842W1_PEA PRELIMINARY; PRT; 488 AA.
AC Q842W1_PEA
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Ent-kaurenoic acid oxidase.
GN Name=KA01;
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
ON NCBI_TaxID=3888;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Shoot;
RX MEDLINE=2241727; PubMed=12529541; DOI=10.1104/pp.012963;
RA Davidson S.E., Elliott R.C., Helliwell C.A., Poole A.T., Reid J.B.;
RT "The pea gene NA encodes ent-kaurenoic acid oxidase.";
RL Plant Physiol. 131:335-344(2003)
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum (By
CC similarity).
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: AF537321; AA023063.1; -; mRNA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0020037; F:heme binding; IEA.
DR GO: GO:0005506; F:iron ion binding; IEA.
DR GO: GO:0046872; F:metal ion binding; IEA.
DR GO: GO:0004497; F:monooxygenase activity; IEA.
```

```
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR001128; Cytochrome_P450.
DR InterPro: IPR002401; EP4501.
DR PANTHER: PTHR19383; Cytochrome_P450; 1.
DR Pfam: PF00067; P450; 2.
DR PRINTS: PR00463; EP4501.
DR PRINTS: PR00385; P450.
DR PROSITE: PS00086; CYTOCHROME_P450; UNKNOWN 1.
KW Endoplasmic reticulum; Heme; Iron; Membrane; Metal-binding;
KW Monooxygenase; Oxidoreductase.
SQ SEQUENCE 488 AA; 56478 MW; 503453CB6B43C830 CRC64;

Query Match 54.1%; Score 53; DB 2; Length 488;
Best Local Similarity 75.0%; Pred. No. 9.5;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 FIGSIWRFLRAF 16
DB 54 FIGWMSFLRAF 65

RESULT 4
Q9F7V7_RHLV PRELIMINARY; PRT; 735 AA.
AC Q9F7V7_RHLV
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE ABC transporter RzcB.
GN Name=rzcB;
OS Rhizobium leguminosarum bv. viciae.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium.
ON NCBI_TaxID=387;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=305;
RX MEDLINE=21360352; PubMed=11467725; DOI=10.1139/cjm-47-6-495;
RA Venter A.P., Twelker S., Oresnik I.J., Hynes M.F.;
RT "Analysis of the genetic region encoding a novel rhizobiocin from
RT Rhizobium leguminosarum bv. viciae strain 305.";
RL Can. J. Microbiol. 47:495-502(2001).
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL: AF273216; AG25076.1; -; Genomic_DNA.
DR HSP; P08716; 1MT0.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0016887; F:ATPase activity; IEA.
DR GO: GO:0042626; F:ATPase activity, coupled to transmembrane m. .; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.
DR GO: GO:0008233; F:peptidase activity; IEA.
DR GO: GO:0008565; F:protein transporter activity; IEA.
DR GO: GO:0015031; P:protein transport; IEA.
DR GO: GO:0006508; P:proteolysis; IEA.
DR InterPro: IPR003593; AAA_AtPase.
DR InterPro: IPR011527; ABC_TM 1.
DR InterPro: IPR001140; ABC_TM transp.
DR InterPro: IPR003439; ABC_transp.like.
DR InterPro: IPR005074; Peptidase_C39.
DR InterPro: IPR010132; Type_I_sec_HlyB.
DR PANTHER: PTHR19242:SF74; Type_I_sec_HlyB; 1.
DR Pfam: PF00664; ABC_membrane; 1.
DR Pfam: PF03412; Peptidase_C39; 1.
DR ProDom: PD000006; ABC_transporter; 1.
DR SMART: SM00382; AAA; 1.
DR TIGRFAMs: TIGR01846; type_I_sec_HlyB; 1.
DR PROSITE: PS50929; ABC_TM1F; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER 1; 1.
DR PROSITE: PS50893; ABC_TRANSPORTER_2; 1.
```

```

DR PROSITE; PS00990; PEPTIDASE_C39; 1.
SQ SEQUENCE 735 AA; 80717 MW; 0216259241F3630C CRC64;

Query Match 52.0%; Score 51; DB 2; Length 735;
Best Local Similarity 56.2%; Pred. No. 30;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRRFGISWRFLRAF 16
   |||:||||:
Db 161 GFWFLPAWRYRAF 176

RESULT 5
Q2NUB5_SODGL PRELIMINARY; PRT; 361 AA.
AC Q2NUB5_SODGL
DT 07-FEB-2006, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DE 07-MAR-2006, entry version 2.
DE Putative glycosyltransferase.
GN ORFNAMES=SG0985;
OS Sodalis glossinidius str. 'morsitans'.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Sodalis.
OC NCBI_TaxID=343509;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Morsitans;
RA Toh H., Weiss B.L., Perkin S.A.H., Yamashita A., Oshima K.,
RA Hattori M., Aksoy S.;
RT "Massive genome erosion and functional adaptations provide insights
RT into the symbiotic lifestyle of Sodalis glossinidius in the tsetse
RT host.";
RL Genome Res. 16:149-156(2006).

CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AP008232; BAE74260.1; -; Genomic_DNA.
DR Transferase.
KW SEQUENCE 361 AA; 40247 MW; 1257F70F3C3CA65C CRC64;

Query Match 51.0%; Score 50; DB 2; Length 361;
Best Local Similarity 69.2%; Pred. No. 21;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 RFIGSIRWFLRAF 16
   |||:||||:
Db 62 RDVGSFWRFLSAF 74

RESULT 6
XKR7_HUMAN STANDARD; PRT; 579 AA.
ID XKR7_HUMAN
AC QSGH72; Q9NUG5;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE XK-related protein 7.
DE Name=XKR7; Synonym=C20orf159, XRG7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
[1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Huang C.-H., Chen Y.;
RT "A superfamily of XK-related genes (XRG) widely expressed in
RT vertebrates and invertebrates.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

```

```

RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.V., Clee C.M.,
RA Clegg S., Copley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhali P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights K., Laird G.K., Lawlor S.,
RA LeHvaslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.D., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,
RA Whittaker P., Willey D.L., Williams L., Williams D.R., Beck S.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
CC (Potential).
CC -!- SIMILARITY: Belongs to the XK family.
CC -!- CAUTION: Ref.2 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AY534245; AAT07094.1; -; mRNA.
DR EMBL; AL031658; CAB88102.1; ALT SEQ; Genomic_DNA.
DR Ensembl; ENSG00000101321; Homo sapiens.
DR HGNC; HGNC:23062; XKR7.
KW Membrane; Transmembrane.
CHAIN 1 579
FT TRANSMEM 59 79
FT TRANSMEM 89 109
FT TRANSMEM 260 280
FT TRANSMEM 314 334
FT TRANSMEM 355 375
FT TRANSMEM 384 404
FT TRANSMEM 415 435
SQ SEQUENCE 579 AA; 63826 MW; D8D0FF64B9ED53D CRC64;

Query Match 51.0%; Score 50; DB 1; Length 579;
Best Local Similarity 58.3%; Pred. No. 34;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 IGSIRWFLRAF 17
   |||:||||:
Db 190 LGQVWRYRALY 201

RESULT 7
XKR7_PANTR STANDARD; PRT; 579 AA.
ID XKR7_PANTR
AC Q49LS1;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE XK-related protein 7.
DE Name=XKR7; Synonym=XRG7;
OS Pan troglodytes (Chimpanzee).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RA NUCLEOTIDE SEQUENCE [MRNA].
 RP Huang C.-H., Chen Y.;
 RT "A superfamily of XK-related genes (XRG) widely expressed in
 vertebrates and invertebrates.";
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
 CC (Potential).
 CC -1- SIMILARITY: Belongs to the XK family.
 CC
 CC Copyrighted by the Uniprot Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AY702910; AAV83783.1; -; mRNA.
 KW Membrane; Transmembrane.
 FT CHAIN 1 579
 FT TRANSMEM 59 79
 FT TRANSMEM 89 109
 FT TRANSMEM 260 280
 FT TRANSMEM 314 334
 FT TRANSMEM 355 375
 FT TRANSMEM 384 404
 FT TRANSMEM 415 435
 FT TRANSMEM 579 AA; 63593 MW; 6DFE1191093E85D4 CRC64;
 SQ SEQUENCE 579 AA; 63593 MW; 6DFE1191093E85D4 CRC64;
 Query Match 51.0%; Score 50; DB 1; Length 579;
 Best Local Similarity 58.3%; Pred. No. 34;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 6 IGSWRFPLAFY 17
 Db 190 LGQVWRYLRALY 201
 RESULT 8
 XKR7 MOUSE STANDARD; PRT; 580 AA.
 ID -XKR7 MOUSE
 AC Q5GH64;
 DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 10.
 DE XK-related protein 7.
 GN Name=Xkr7; Synonyms=Xrg7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RA Huang C.-H., Chen Y.;
 RT "A superfamily of XK-related genes (XRG) widely expressed in
 vertebrates and invertebrates.";
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
 CC (Potential).
 CC -1- SIMILARITY: Belongs to the XK family.
 CC
 CC Copyrighted by the Uniprot Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AY534253; AAT07102.1; -; mRNA.
 DR Ensembl; ENSMUSG00000042631; Mus musculus.
 DR MGI; MGI:3526711; Xkr7.
 KW Membrane; Transmembrane.
 FT CHAIN 1 580
 FT TRANSMEM 59 79
 FT TRANSMEM 89 109
 FT TRANSMEM 260 280
 FT TRANSMEM 303 323
 FT TRANSMEM 326 346
 FT TRANSMEM 355 375
 FT TRANSMEM 384 404
 FT TRANSMEM 415 435
 FT TRANSMEM 580 AA; 64302 MW; F3291FABF4C5A826 CRC64;
 SQ SEQUENCE 580 AA; 64302 MW; F3291FABF4C5A826 CRC64;
 Query Match 51.0%; Score 50; DB 1; Length 580;
 Best Local Similarity 58.3%; Pred. No. 34;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 6 IGSWRFPLAFY 17
 Db 190 LGQVWRYLRALY 201
 RESULT 9
 XKR7 RAT STANDARD; PRT; 580 AA.
 ID -XKR7 RAT
 AC Q5GH56;
 DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE XK-related protein 7.
 GN Name=Xkr7; Synonyms=Xrg7;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RA Huang C.-H., Chen Y.;
 RT "A superfamily of XK-related genes (XRG) widely expressed in
 vertebrates and invertebrates.";
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
 CC (Potential).
 CC -1- SIMILARITY: Belongs to the XK family.
 CC
 CC Copyrighted by the Uniprot Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AY534261; AAT07110.1; -; mRNA.
 KW Membrane; Transmembrane.
 FT CHAIN 1 580
 FT TRANSMEM 59 79
 FT TRANSMEM 89 109
 FT TRANSMEM 260 280
 FT TRANSMEM 303 323
 FT TRANSMEM 326 346
 FT TRANSMEM 355 375
 FT TRANSMEM 384 404
 FT TRANSMEM 415 435
 FT TRANSMEM 580 AA; 64338 MW; 8F4907F391B4F59E CRC64;
 SQ SEQUENCE 580 AA; 64338 MW; 8F4907F391B4F59E CRC64;
 Query Match 51.0%; Score 50; DB 1; Length 580;
 Best Local Similarity 58.3%; Pred. No. 34;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 6 IGSWRFPLAFY 17
 Db 190 LGQVWRYLRALY 201
 RESULT 10
 Q7VV93 BORPE PRELIMINARY; PRT; 278 AA.
 ID Q7VV93 BORPE
 AC Q7VV93;
 FT TRANSMEM 59 79
 FT TRANSMEM 89 109
 FT TRANSMEM 260 280
 FT TRANSMEM 303 323
 FT TRANSMEM 326 346
 FT TRANSMEM 355 375
 FT TRANSMEM 384 404
 FT TRANSMEM 415 435
 FT TRANSMEM 580 AA; 64302 MW; F3291FABF4C5A826 CRC64;
 SQ SEQUENCE 580 AA; 64302 MW; F3291FABF4C5A826 CRC64;

FT TRANSMEM 89 109 Potential.
 FT TRANSMEM 260 280 Potential.
 FT TRANSMEM 303 323 Potential.
 FT TRANSMEM 326 346 Potential.
 FT TRANSMEM 355 375 Potential.
 FT TRANSMEM 384 404 Potential.
 FT TRANSMEM 415 435 Potential.
 SQ SEQUENCE 580 AA; 64302 MW; F3291FABF4C5A826 CRC64;
 Query Match 51.0%; Score 50; DB 1; Length 580;
 Best Local Similarity 58.3%; Pred. No. 34;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 6 IGSWRFPLAFY 17
 Db 190 LGQVWRYLRALY 201
 RESULT 9
 XKR7 RAT STANDARD; PRT; 580 AA.
 ID -XKR7 RAT
 AC Q5GH56;
 DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE XK-related protein 7.
 GN Name=Xkr7; Synonyms=Xrg7;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muroidae; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RA Huang C.-H., Chen Y.;
 RT "A superfamily of XK-related genes (XRG) widely expressed in
 vertebrates and invertebrates.";
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
 CC (Potential).
 CC -1- SIMILARITY: Belongs to the XK family.
 CC
 CC Copyrighted by the Uniprot Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; AY534261; AAT07110.1; -; mRNA.
 KW Membrane; Transmembrane.
 FT CHAIN 1 580
 FT TRANSMEM 59 79
 FT TRANSMEM 89 109 Potential.
 FT TRANSMEM 260 280 Potential.
 FT TRANSMEM 303 323 Potential.
 FT TRANSMEM 326 346 Potential.
 FT TRANSMEM 355 375 Potential.
 FT TRANSMEM 384 404 Potential.
 FT TRANSMEM 415 435 Potential.
 FT TRANSMEM 580 AA; 64338 MW; 8F4907F391B4F59E CRC64;
 SQ SEQUENCE 580 AA; 64338 MW; 8F4907F391B4F59E CRC64;
 Query Match 51.0%; Score 50; DB 1; Length 580;
 Best Local Similarity 58.3%; Pred. No. 34;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 6 IGSWRFPLAFY 17
 Db 190 LGQVWRYLRALY 201
 RESULT 10
 Q7VV93 BORPE PRELIMINARY; PRT; 278 AA.
 ID Q7VV93 BORPE
 AC Q7VV93;
 FT TRANSMEM 59 79
 FT TRANSMEM 89 109
 FT TRANSMEM 260 280
 FT TRANSMEM 303 323
 FT TRANSMEM 326 346
 FT TRANSMEM 355 375
 FT TRANSMEM 384 404
 FT TRANSMEM 415 435
 FT TRANSMEM 580 AA; 64302 MW; F3291FABF4C5A826 CRC64;
 SQ SEQUENCE 580 AA; 64302 MW; F3291FABF4C5A826 CRC64;

RA	Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K., Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Unwin L., Whitehead S., Barrell B.G., Maskell D.J.; "Comparative analysis of the genome sequences of Bordetella pertussis, RT Bordetella parapertussis and Bordetella bronchiseptica."; Nat. Genet. 35:32-40(2003).	CC
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License	CC
CC	EMBL; BX604430; CAE37766.1; -; Genomic_DNA.	CC
DR	BioCyc; BPAR519:BPP2471-MONOMER; -.	DR
DR	GO; GO:0005524; F:ATP binding; IEA.	DR
DR	GO; GO:0004672; P:protein kinase activity; IEA.	DR
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.	DR
DR	InterPro; IPR000719; Prot_Kinase.	DR
DR	ProDom; PD000001; Prot_Kinase; 1.	DR
KW	Complete proteome; Hypothetical protein; Kinase; Transferase.	KW
SEQUENCE	278 AA; 31565 MW; 11DDFD84EPEEF8DF CRC64;	SEQUENCE
Query Match	50.0%; Score 49; DB 2; Length 278;	
Best Local Similarity	52.9%; Pred. No. 23;	
Matches	9; Conservative 4; Mismatches 4; Indels 0; Gaps	
QY	1 GIRREIGSIWFLRAFY 17	
DB	S:	
	47 GVRRGISVLYLRRAFF 63	
RESULT 12		
Q7WLJ3.BORBR		
ID	Q7WLJ3.BORBR PRELIMINARY; PRT; 278 AA.	
AC	Q7WLJ31;	
DT	01-OCT-2003, integrated into UniProtKB/TrEMBL.	
DT	01-OCT-2003, sequence version 1.	
DT	21-FEB-2006, entry version 14.	
DE	Hypothetical protein.	
GN	OrderedLocustNames=BB1918;	
OS	Bordetella bronchiseptica (Alcaligenes bronchisepticus).	
OC	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;	
OC	Alcaligenaceae; Bordetella.	
ON	NCBI_TaxID=518;	
OX	[1]	
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	
RC	STRAIN=RB50 / ATCC EAA-586;	
RC	MEDLINE=22827954; PubMed=42910271; DOI=10.1038/ngl1227;	
RA	Parikhall J., Sebahia M., Preston A., Murphy L.D., Thomson N.R., Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L., Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A., Achtman M., Atkin R., Baker S., Basham D., Baeson N., Chervach I., Chillingworth T., Collins S., Cronin A., Davis P., Doggett J., Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jageis K., Leather S., Moule S., Norbertczak H., O'Neill S., Ormond D., Price C., Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K., Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Unwin L., Whitehead S., Barrell B.G., Maskell D.J.	
RT	"Comparative analysis of the genome sequences of Bordetella pertussis, RT Bordetella parapertussis and Bordetella bronchiseptica."; Nat. Genet. 35:32-40(2003).	
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License	CC
CC	EMBL; BX604430; CAE32415.1; -; Genomic_DNA.	CC
DR	BioCyc; BBRO518:BB1918-MONOMER; -.	DR
DR	GO; GO:0005524; F:ATP binding; IEA.	DR
DR	GO; GO:0004672; P:protein kinase activity; IEA.	DR
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.	DR
DR	InterPro; IPR000719; Prot_Kinase.	DR
DR	ProDom; PD000001; Prot_Kinase; 1.	DR
KW	Complete proteome; Hypothetical protein; Kinase; Transferase.	KW
SEQUENCE	278 AA; 31507 MW; 66DDBEF1D728D768 CRC64;	SEQUENCE

```

Query Match          50.0%; Score 49; DB 2; Length 278;
Best Local Similarity 52.9%; Pred. No. 23;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRRFIGSIWRFRAF 17
   ||| : ||| : ||| :
Db 47 GVRGSIYVLRRAFF 63

RESULT 13
Q39L57 BURS3
ID Q39L57_BURS3 PRELIMINARY; PRT; 407 AA.
AC Q39L57
DT 22-NOV-2005, integrated into UniProtKB/TrEMBL.
DT 21-FEB-2006, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein.
GN OrderedLocusNames=Bcep18194_A3207;
OS Burkholderia sp. (strain 383) (Burkholderia cepacia (strain ATCC 17760
/ NCIB 9086 / R18194)).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OC NCBI_TaxID=269483;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG US DOE Joint Genome Institute;
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Chain P., Malfatti S., Shin M.,
RA Vergez L., Schmutz J., Larimer F., Land M., Kyrpides N., Lykidis A.,
RA Richardson P.;
RT "Complete sequence of chromosome 1 of Burkholderia sp. 383.";
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; CP000151; AB506809.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 407 AA; 45483 MW; 957829B27BCABFC1 CRC64;

Query Match          50.0%; Score 49; DB 2; Length 407;
Best Local Similarity 41.2%; Pred. No. 35;
Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRRFIGSIWRFRAF 17
   ||| : ||| : ||| :
Db 327 GIRQMLGHVQWTRSS 343

RESULT 14
Q456F4_9BURK
ID Q456F4_9BURK PRELIMINARY; PRT; 408 AA.
AC Q456F4;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Hypothetical protein.
GN ORFNames=BcenDRAFT_3751;
OS Burkholderia cenocepacia AU 1054.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OC NCBI_TaxID=331271;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG STRAIN=AU 1054;
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
AU 1054.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.

```

```

RC STRAIN=AU 1054;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
AU 1054.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AAH01000010; EAM12352.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 408 AA; 45545 MW; 3C2BCA9471BAAE93 CRC64;

Query Match          50.0%; Score 49; DB 2; Length 408;
Best Local Similarity 41.2%; Pred. No. 35;
Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRRFIGSIWRFRAF 17
   ||| : ||| : ||| :
Db 328 GIRQMLGHVQWTRSS 344

RESULT 15
Q4LK44_9BURK
ID Q4LK44_9BURK PRELIMINARY; PRT; 408 AA.
AC Q4LK44;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Hypothetical protein.
GN ORFNames=Bcen2424DRAFT_1071;
OS Burkholderia cenocepacia HI2424.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OC NCBI_TaxID=331272;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG STRAIN=HI2424;
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
HI2424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG STRAIN=HI2424;
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
HI2424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AAHL01000063; EAM16412.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 408 AA; 45603 MW; 7F393888305911D2 CRC64;

Query Match          50.0%; Score 49; DB 2; Length 408;
Best Local Similarity 41.2%; Pred. No. 35;
Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 GIRRFIGSIWRFRAF 17
   ||| : ||| : ||| :

```

Db 328 GIRQMLGHVWQWTRSSY 344

Search completed: May 19, 2006, 14:38:13
Job time : 116.429 secs

This Page Blank (usp10)


```
Query Match          75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 4.8e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 G1RRFIGSIWRFLRAFYG 18
   ||::|||::|||::|||
Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 2
US-08-940-093-242
; Sequence 242, Application US/08940093
; Patent No. 6037323
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,093
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6037323e
; US-08-940-093-242

Query Match          75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 4.8e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 G1RRFIGSIWRFLRAFYG 18
   ||::|||::|||::|||
Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 3
US-08-940-096-242
; Sequence 242, Application US/08940096
; Patent No. 6046166
; GENERAL INFORMATION:
```

```
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,096
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0005-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6046166e
; US-08-940-096-242

Query Match          75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 4.8e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 G1RRFIGSIWRFLRAFYG 18
   ||::|||::|||::|||
Db 1 G1KKFLGSIWKFIKAFVG 18

RESULT 4
US-09-465-719-242
; Sequence 242, Application US/09465719
; Patent No. 6265377
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
```

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/465,719
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,093
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0006-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6265377e
; US-09-465-719-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 4.8e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFFIGSIWRFLRAFGV 18
||::|||::|||
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 5
US-09-453-605-242
; Sequence 242, Application US/09453605
; Patent No. 6329341
; GENERAL INFORMATION:
; APPLICANT: Daseux, Jean-Louis
; Sekul, Renate
; Buttner, Klaus
; Cornut, Isabelle
; Metz, Gunther
; Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,605
; FILING DATE: 26-NO. 6329341-1999
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
```

```
;
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6329341e
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:
; US-09-453-605-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 4.8e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRFFIGSIWRFLRAFGV 18
||::|||::|||
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 6
US-09-453-838-242
; Sequence 242, Application US/09453838
; Patent No. 6376464
; GENERAL INFORMATION:
; APPLICANT: Daseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,838
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6376464e
```

```
US-09-453-838-242
Query Match          75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 4.8e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFGSIWRFLEAFVG 18
   ||:::||:::||:::||
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 7
US-08-940-136-242
; Sequence 242, Application US/08940136
; Patent No. 6518412
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; TITLE OF INVENTION: SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/940,136
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0007-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6518412e
; US-08-940-136-242

Query Match          75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 4.8e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFGSIWRFLEAFVG 18
   ||:::||:::||:::||
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 8
US-09-453-841-242
; Sequence 242, Application US/09453841
; Patent No. 6573239
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,841
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 009196-0004-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6573239e
; US-09-453-841-242

Query Match          75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 4.8e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 GIRRFGSIWRFLEAFYG 18
   ||:::||:::||:::||
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 9
US-09-453-833-242
; Sequence 242, Application US/09453833
; Patent No. 6602854
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
```

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA: US/09/453,833
APPLICATION NUMBER: US/09/453,833
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6602854e
US-09-453-833-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 4.8e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFIGSIWRFLEAFYG 18
Db 1 GIKKFLGSIWKFIFAFVG 18

RESULT 10
US-09-453-826-242
Sequence 242, Application US/09453826
Patent No. 6630450
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,826
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6630450e
US-09-453-826-242

Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 4.8e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFIGSIWRFLEAFYG 18
Db 1 GIKKFLGSIWKFIFAFVG 18

RESULT 11
US-09-453-840-242
Sequence 242, Application US/09453840
Patent No. 6716816
GENERAL INFORMATION:
APPLICANT: Dasseux, Jean-Louis
APPLICANT: Sekul, Renate
APPLICANT: Buttner, Klaus
APPLICANT: Cornut, Isabelle
APPLICANT: Metz, Gunther
APPLICANT: Dufourcq, Jean
TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
TITLE OF INVENTION: AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,840
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/940,095
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 009196-0004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 242:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids

```
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6716816e
US-09-453-840-242
Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 4.8e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFISIWRFLEAFYG 18
|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 12
US-09-865-989-242
; Sequence 242, Application US/09865989
; Patent No. 6734169
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 25-May-2001
; FILING DATE: 25-May-2001
; CLASSIFICATION:
; APPLICATION NUMBER: 09/465,719
; FILING DATE: 17-DEC-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6734169e
; SEQUENCE DESCRIPTION: SEQ ID NO: 242:

US-09-865-989-242
Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 4.8e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFISIWRFLEAFYG 18
|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 13
US-09-453-834-242
; Sequence 242, Application US/09453834
; Patent No. 6753313
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: APOLIPOPROTEIN A-I AGONISTS
; AND THEIR USE TO TREAT DYSLIPIDEMIC DISORDERS
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 29-SEP-1997
; FILING DATE: 29-SEP-1997
; CLASSIFICATION:
; APPLICATION NUMBER: 08/940,095
; FILING DATE: 29-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 242:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6753313e
US-09-453-834-242
Query Match 75.5%; Score 74; DB 2; Length 18;
Best Local Similarity 61.1%; Pred. No. 4.8e-05;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFISIWRFLEAFYG 18
|:::|:::|:::|
Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 14
US-10-283-599-242
; Sequence 242, Application US/10283599
; Patent No. 684327
; GENERAL INFORMATION:
; APPLICANT: Dasseux, Jean-Louis
; APPLICANT: Sekul, Renate
; APPLICANT: Buttner, Klaus
; APPLICANT: Cornut, Isabelle
; APPLICANT: Metz, Gunther
; APPLICANT: Dufourcq, Jean
; TITLE OF INVENTION: GENE THERAPY APPROACHES TO
; SUPPLY APOLIPOPROTEIN A-I AGONISTS AND THEIR
```

; TITLE OF INVENTION: USE TO TREAT DYSLIPIDEMIC DISORDERS.

; NUMBER OF SEQUENCES: 274

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036-2811

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/283,599

; FILING DATE: 29-OCT-2002

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/940,136

; FILING DATE: 29-SEP-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 009196-0007-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-493-4935

; TELEFAX: 650-493-5556

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 242:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: No. 6844327e

; US-10-283-599-242

Query Match

Best Local Similarity 75.5%; Score 74; DB 2; Length 18;

Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFIGSIWRFLRAFYG 18

Db 1 GIKKFLGSIWKFIKAFVG 18

RESULT 15

US-09-465-718-242

; Sequence 242, Application US/09465718

; Patent No. 6900177

; GENERAL INFORMATION:

; APPLICANT: Dasseux, Jean-Louis

; APPLICANT: Sekul, Renate

; APPLICANT: Buttner, Klaus

; APPLICANT: Cornut, Isabelle

; APPLICANT: Metz, Gunther

; TITLE OF INVENTION: APOLIPROTEIN A-I AGONISTS

; NUMBER OF SEQUENCES: 258

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036-2811

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/465,718

; FILING DATE: 17-Dec-1999

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/940,096

; FILING DATE: 29-SEP-1997

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 009196-0005-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-493-4935

; TELEFAX: 650-493-5556

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 242:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: No. 6900177e

; US-09-465-718-242

Query Match

Best Local Similarity 75.5%; Score 74; DB 2; Length 18;

Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GIRRFIGSIWRFLRAFYG 18

Db 1 GIKKFLGSIWKFIKAFVG 18

Search completed: May 19, 2006, 14:42:55

Job time : 25.8571 secs

This Page Blank (usp10)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 15:18:19 ; Search time 81.2857 Seconds
(without alignments)
102.575 Million cell updates/sec

Title: US-10-712-447-117

Perfect score: 98

Sequence: 1 GIRFIGSIWRFLRAFG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA_Main.*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pgp.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pgp.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pgp.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pgp.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pgp.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pgp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	98	100.0	18	4	US-10-712-447-117
2	94	95.9	18	4	US-10-712-447-2
3	94	95.9	18	4	US-10-712-447-5
4	94	95.9	18	4	US-10-712-447-8
5	94	95.9	18	4	US-10-712-447-10
6	94	95.9	18	4	US-10-712-447-13
7	94	95.9	18	4	US-10-712-447-115
8	94	95.9	18	4	US-10-712-447-116
9	94	95.9	18	4	US-10-712-447-127
10	94	95.9	18	4	US-10-712-447-129
11	94	95.9	18	4	US-10-712-447-131
12	91	92.9	18	4	US-10-712-447-91
13	88	89.8	18	4	US-10-712-447-21
14	88	89.8	18	4	US-10-712-447-53
15	88	89.8	18	4	US-10-712-447-74
16	86	87.8	18	4	US-10-712-447-4
17	86	87.8	18	4	US-10-712-447-113
18	85	86.7	18	4	US-10-712-447-99
19	84	85.7	18	4	US-10-712-447-18
20	84	85.7	18	4	US-10-712-447-112
21	84	85.7	18	4	US-10-712-447-114
22	83	84.7	18	4	US-10-712-447-17
23	83	84.7	18	4	US-10-712-447-121
24	82	83.7	18	4	US-10-712-447-61
25	82	83.7	18	4	US-10-712-447-82
26	81	82.7	18	4	US-10-712-447-16
27	81	82.7	18	4	US-10-712-447-96

Sequence 22, Appl
Sequence 78, Appl
Sequence 95, Appl
Sequence 120, Appl
Sequence 19, Appl
Sequence 56, Appl
Sequence 58, Appl
Sequence 77, Appl
Sequence 79, Appl
Sequence 80, Appl
Sequence 84, Appl
Sequence 57, Appl
Sequence 100, Appl
Sequence 41, Appl
Sequence 110, Appl
Sequence 118, Appl
Sequence 97, Appl
Sequence 242, Appl

ALIGNMENTS

RESULT 1

US-10-712-447-117
; Sequence 117, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GABER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 117
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-117

Query Match 100.0%; Score 98; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.2e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRFIGSIWRFLRAFG 18
Db 1 GIRFIGSIWRFLRAFG 18

RESULT 2

US-10-712-447-2
; Sequence 2, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GABER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13

```
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; OTHER INFORMATION: c-term amidated
US-10-712-447-2

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFSGSIWRFLRAFYG 18
Db 1 GIRFLGSIWRFLRAFYG 18

RESULT 3
US-10-712-447-5
; Sequence 5, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-5

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFSGSIWRFLRAFYG 18
Db 1 GIRFLGSIWRFLRAFYG 18

RESULT 4
US-10-712-447-8
; Sequence 8, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-8

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFSGSIWRFLRAFYG 18
Db 1 GIRFLGSIWRFLRAFYG 18

RESULT 5
US-10-712-447-10
; Sequence 10, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-10

Query Match          95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIRRFSGSIWRFLRAFYG 18
Db 1 GIRFLGSIWRFLRAFYG 18

RESULT 6
US-10-712-447-13
; Sequence 13, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 18
```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-13

Query Match 95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRFIGSIWRFLRAFYG 18
|:|||||:|||||
Db 1 GRRFLGSIWRFLRAFYG 18

RESULT 7
US-10-712-447-115
; Sequence 115, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 115
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-115

Query Match 95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRFIGSIWRFLRAFYG 18
|:|||||:|||||
Db 1 GLRRFIGSIWRFLRAFYG 18

RESULT 8
US-10-712-447-116
; Sequence 116, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 116
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-116

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-116

Query Match 95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRFIGSIWRFLRAFYG 18
|:|||||:|||||
Db 1 GLRRFIGSIWRFLRAFYG 18

RESULT 9
US-10-712-447-127
; Sequence 127, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 127
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-127

Query Match 95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GRRFIGSIWRFLRAFYG 18
|:|||||:|||||
Db 1 GLRRFIGSIWRFLRAFYG 18

RESULT 10
US-10-712-447-129
; Sequence 129, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712,447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 129
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-129

Query Match 95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFIGSIWRFLRAFYG 18
| | | | | | | | | | | | | | | | | |
Db 1 GRRFLGSLWRFLRAFYG 18

RESULT 11
US-10-712-447-131
; Sequence 131, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 131
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-131

Query Match 95.9%; Score 94; DB 4; Length 18;
Best Local Similarity 88.9%; Pred. No. 3.7e-07;
Matches 16; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFIGSIWRFLRAFYG 18
| | | | | | | | | | | | | | | | | |
Db 1 GLRRFLGSIWRFLRAFYG 18

RESULT 12
US-10-712-447-91
; Sequence 91, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 91
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-91

Query Match 92.9%; Score 91; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. No. 1e-06;

Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFIGSIWRFLRAFYG 18
| | | | | | | | | | | | | | | | | |
Db 1 GRRFLGSIWRFLRAFYG 18

RESULT 13
US-10-712-447-21
; Sequence 21, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 21
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-21

Query Match 89.8%; Score 88; DB 4; Length 18;
Best Local Similarity 77.8%; Pred. No. 3e-06;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GRRFIGSIWRFLRAFYG 18
| | | | | | | | | | | | | | | | | |
Db 1 GRRFLGSIWRFLRAFYG 18

RESULT 14
US-10-712-447-53
; Sequence 53, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 53
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; NAME/KEY: MOD RES
; LOCATION: (3)
; OTHER INFORMATION: (DiMe)Lys
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (14)

Tue May 23 08:37:59 2006

```
; OTHER INFORMATION: (Dime)Lys
US-10-712-447-53
Query Match      89.8%; Score 88; DB 4; Length 18;
Best Local Similarity 77.8%; Pred.No. 3e-06;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GRRFIGSIWRFLRAFYG 18
      |||:|||:|||:|||
Db      1 GKRFLGSIWRFLRAFYG 18

RESULT 15
US-10-712-447-74
; Sequence 74, Application US/10712447
; Publication No. US20040186057A1
; GENERAL INFORMATION:
; APPLICANT: ANANTHARAMIAH, GATTADAHALLI M.
; APPLICANT: GARBER, DAVID W.
; APPLICANT: DATTA, GEETA
; TITLE OF INVENTION: SYNTHETIC SINGLE DOMAIN POLYPEPTIDES MIMICKING
; TITLE OF INVENTION: APOLIPOPROTEIN E AND METHODS OF USE
; FILE REFERENCE: 112739-123US
; CURRENT APPLICATION NUMBER: US/10/712.447
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 60/425,821
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 74
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-712-447-74
Query Match      89.8%; Score 88; DB 4; Length 18;
Best Local Similarity 77.8%; Pred.No. 3e-06;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GRRFIGSIWRFLRAFYG 18
      |||:|||:|||:|||
Db      1 GKRFLGSIWRFLRAFYG 18
```

Search completed: May 19, 2006, 15:27:57
Job time : 82.2857 secs

This Page Blank (uspto)

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2006, 15:18:37 ; Search time 2.14286 seconds
(without alignments)
17.943 Million cell updates/sec

Title: US-10-712-447-117

Perfect score: 98

Sequence: 1 GIRRFISIWFLRAFYG 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 21570 seqs, 2136119 residues

Total number of hits satisfying chosen parameters: 21570

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:

- 1: /EMC Celleria_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.psp:**
- 2: /EMC Celleria_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.psp:**
- 3: /EMC Celleria_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.psp:**
- 4: /EMC Celleria_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.psp:**
- 5: /EMC Celleria_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.psp:**
- 6: /EMC Celleria_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.psp:**
- 7: /EMC Celleria_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.psp:**
- 8: /EMC Celleria_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.psp:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37.5	38.3	441	6	US-10-511-937-2947
2	36	36.7	74	1	US-09-949-925-111
3	35	35.7	313	7	US-11-242-505A-48
4	35	35.7	342	7	US-11-204-427-7
5	35	35.7	403	7	US-11-242-505A-18
6	35	35.7	667	7	US-11-311-555-16
7	35	35.7	667	7	US-11-311-561-16
8	35	35.7	764	7	US-11-223-738-6
9	34	34.7	447	6	US-10-975-692-2
10	34	34.7	599	7	US-11-302-678-5
11	34	34.7	627	7	US-11-249-111-88
12	33	33.7	643	6	US-10-504-120-19
13	33	33.7	651	6	US-10-511-937-2401
14	33	33.7	714	6	US-10-868-498-2
15	33	33.7	749	6	US-10-505-928-443
16	33	33.7	919	7	US-11-302-678-62
17	32.5	33.2	60	1	US-09-949-925-142
18	32.5	33.2	4590	6	US-10-505-928-569
19	32	32.7	351	6	US-10-511-937-2540
20	32	32.7	364	7	US-11-113-081A-6
21	32	32.7	388	6	US-10-196-749-336
22	32	32.7	388	7	US-11-024-544A-169
23	32	32.7	388	7	US-11-190-750-137
24	32	32.7	388	7	US-11-204-427-1
25	32	32.7	393	7	US-11-304-129-40

Sequence 48, Appl
Sequence 2993, Ap
Sequence 543, App
Sequence 274, App
Sequence 18, Appl
Sequence 674, App
Sequence 12, Appl
Sequence 21, Appl
Sequence 135, App
Sequence 87, Appl
Sequence 23, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 3, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 26, Appl
Sequence 6, Appl
Sequence 2530, Ap

US-10-511-937-2947
Sequence 2947, Application US/10511937
Publication No. US2006008836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fy, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, Macdonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2947
LENGTH: 441
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-937-2947

Query Match 38.3%; Score 37.5; DB 6; Length 441;
Best Local Similarity 33.3%; Pred. No. 13;
Matches 7; Conservative 5; Mismatches 6; Indels 3; Gaps 1;

Oy 1 GIRRFISIW---RFLRAFYG 18
| : : : : :
Db 106 GLSKFLGTHLMGNILRLFLG 126

RESULT 2
US-09-949-925-111
Sequence 111, Application US/09949925
Publication No. US20060099575A9
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 67 Human secreted proteins

ALIGNMENTS

RESULT 1
US-10-511-937-2947
Sequence 2947, Application US/10511937
Publication No. US2006008836A1
GENERAL INFORMATION:
APPLICANT: EXPRESSION DIAGNOSTICS, INC.
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fy, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, Macdonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 3117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2947
LENGTH: 441
TYPE: PRT
ORGANISM: Homo sapiens
US-10-511-937-2947

Query Match 38.3%; Score 37.5; DB 6; Length 441;
Best Local Similarity 33.3%; Pred. No. 13;
Matches 7; Conservative 5; Mismatches 6; Indels 3; Gaps 1;

Oy 1 GIRRFISIW---RFLRAFYG 18
| : : : : :
Db 106 GLSKFLGTHLMGNILRLFLG 126

RESULT 2
US-09-949-925-111
Sequence 111, Application US/09949925
Publication No. US20060099575A9
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 67 Human secreted proteins

```
; FILE REFERENCE: PZ023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (74)
; OTHER INFORMATION: Xaa equals stop translation
US-09-949-925-111
```

```
Query Match 36.7%; Score 36; DB 1; Length 74;
Best Local Similarity 54.5%; Pred. No. 2.8;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

QY 2 IRRFIGSIWRF 12

Db 59 LREVGKIWRF 69

```
RESULT 3
US-11-242-505A-48
; Sequence 48, Application US/11242505A
; Publication No. US20060099656A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
; FILE REFERENCE: MPI2001-288P1RCP10NNIM
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-242-505A-48
```

```
Query Match 36.7%; Score 36; DB 1; Length 74;
Best Local Similarity 54.5%; Pred. No. 2.8;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
Query Match 35.7%; Score 35; DB 7; Length 313;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 10 WRFLRAFY 17

Db 199 WSELDAFY 206

```
RESULT 4
US-11-204-427-7
; Sequence 7, Application US/11204427
; Publication No. US20060100146A1
; GENERAL INFORMATION:
; APPLICANT: Sturley, Stephen L
; APPLICANT: Turkish, Aaron R
; APPLICANT: Billheimer, Jeffrey T
; APPLICANT: Cromley, Debra
; TITLE OF INVENTION: AWAT-RELATED METHODS AND ARTICLES
; FILE REFERENCE: 0575/72796/JPW/AJM/JCS
; CURRENT APPLICATION NUMBER: US/11/204,427
; CURRENT FILING DATE: 2005-08-15
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-204-427-7
```

```
Query Match 35.7%; Score 35; DB 7; Length 342;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

QY 8 SIWRFLRAFY 17

Db 84 AIWRQLRDYV 93

```
RESULT 5
US-11-242-505A-18
; Sequence 18, Application US/11242505A
; Publication No. US20060099656A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
; FILE REFERENCE: MPI2001-288P1RCP10NNIM
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-242-505A-18
```

```
Query Match 35.7%; Score 35; DB 7; Length 403;
Best Local Similarity 44.4%; Pred. No. 32;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

QY 2 IRRFIGSIW 10


```
Db      155 VRRVLGAVW 163
      :||:|:|:|
RESULT 6
US-11-311-555-16
; Sequence 16, Application US/11311555
; Publication No. US20060088916A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1 (US)
; CURRENT APPLICATION NUMBER: US/11/311,555
; CURRENT FILING DATE: 2005-12-20
; PRIOR APPLICATION NUMBER: US/09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 16
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-311-555-16

Query Match      35.7%; Score 35; DB 7; Length 667;
Best Local Similarity 43.8%; Pred. No. 58;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      3 RRFIGSIWRFELAFYG 18
      :||:|:|:|
Db      502 RRLVGALAEELRAALG 517
      :||:|:|:|
RESULT 7
US-11-311-555-16
; Sequence 16, Application US/11311551
; Publication No. US20060088917A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1 (US)
; CURRENT APPLICATION NUMBER: US/11/311,555
; CURRENT FILING DATE: 2005-12-20
; PRIOR APPLICATION NUMBER: US/09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 16
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-311-555-16

Query Match      35.7%; Score 35; DB 7; Length 667;
Best Local Similarity 43.8%; Pred. No. 58;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      3 RRFIGSIWRFELAFYG 18
      :||:|:|:|
Db      502 RRLVGALAEELRAALG 517
      :||:|:|:|
RESULT 8
US-11-223-738-6
; Sequence 6, Application US/11223738
; Publication No. US20060099682A1
; GENERAL INFORMATION:
; APPLICANT: DELANY, Samantha
; APPLICANT: SANSEAU, Philippe
; APPLICANT: TATE, Simon Nicholas
; TITLE OF INVENTION: HUMAN VANILLOID RECEPTORS AND THEIR USES
; FILE REFERENCE: PG3606D1
; CURRENT APPLICATION NUMBER: US/11/223,738
; CURRENT FILING DATE: 2005-09-09
; PRIOR APPLICATION NUMBER: 09/857,123
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: PCT/EP99/09284
; PRIOR FILING DATE: 1999-11-30
```

```
; PRIOR APPLICATION NUMBER: GB98263593
; PRIOR FILING DATE: 1998-12-01
; NUMBER OF SEQ ID NOS: 40
; SEQ ID NO 6
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-223-738-6

Query Match      35.7%; Score 35; DB 7; Length 764;
Best Local Similarity 42.9%; Pred. No. 69;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      1 GIRFTGSIWRF 14
      |||:|:|
Db      443 GYLLVQLMYFWR 456

RESULT 9
US-10-975-692-2
; Sequence 2, Application US/10975692
; Publication No. US20060090221A1
; GENERAL INFORMATION:
; APPLICANT: WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION
; APPLICANT: Browne, John A
; APPLICANT: Wallis, James G
; APPLICANT: Watts, Jennifer L.
; TITLE OF INVENTION: DESATURASES AND METHODS OF USING THEM FOR SYNTHESIS OF
; FILE REFERENCE: 4630-58963-02
; CURRENT APPLICATION NUMBER: US/10/975,692
; CURRENT FILING DATE: 2004-10-26
; PRIOR APPLICATION NUMBER: US 09/857,583
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/28655
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/111,301
; PRIOR FILING DATE: 1998-12-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-975-692-2

Query Match      34.7%; Score 34; DB 6; Length 447;
Best Local Similarity 43.8%; Pred. No. 53;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      2 IRRFTGSIWRF 17
      |||:|:|
Db      130 IRKLETFILFAFY 145

RESULT 10
US-11-302-678-5
; Sequence 5, Application US/11302678
; Publication No. US2006008881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 50899, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12103, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
; FILE REFERENCE: WPI02-012PIRM.OMNI
; CURRENT APPLICATION NUMBER: US/11/302,678
; CURRENT FILING DATE: 2005-12-14
; PRIOR APPLICATION NUMBER: US/10/345,680
; PRIOR FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511

; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-302-678-5

Query Match      34.7%; Score 34; DB 7; Length 599;
Best Local Similarity 57.1%; Pred. No. 76;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      6 IGSIRWF 12
      |:|:|
Db      64 LGNWRWF 70

RESULT 11
US-11-249-111-88
; Sequence 88, Application US/11249111
; Publication No. US20060099623A1
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Dekker, James
; TITLE OF INVENTION: Polynucleotides and polypeptides isolated from Lactobacillus
; FILE REFERENCE: 13353.1048ulc2
; CURRENT APPLICATION NUMBER: US/11/249,111
; CURRENT FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: 10/288,930
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 09/724,623
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/148,801
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 827
; TYPE: PRT
; ORGANISM: Lactobacillus rhamnosus
US-11-249-111-88

Query Match      34.7%; Score 34; DB 7; Length 627;
Best Local Similarity 55.6%; Pred. No. 80;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      5 FIGSIWRF 13
      |:|:|
Db      194 FVGTIWMWL 202

RESULT 12
US-10-504-120-19
; Sequence 19, Application US/10504120
```


Job time : 2.14286 secs

5